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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:27:41 ; Search time 96.8571 Seconds

US-09-868-605-14\_COPY\_113\_121

{without alignments} 33.333 Million cell updates/sec

Title: Perfect score: 1 GIVVIIHQMS 9

Sequence: BIOSUN62 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing First 45 summaries

Database :

A\_Geneseq\_23Sep04: \*  
1: geneseq21980s: \*  
2: geneseq21990s: \*  
3: geneseq22000s: \*  
4: geneseq22010s: \*  
5: geneseq22002s: \*  
6: geneseq22003s: \*  
7: geneseq22004s: \*  
8: geneseq22005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	47	100.0	26	3 AYV5328
2	47	100.0	30	3 AYV5327
3	47	100.0	250	2 AYV5327
4	47	100.0	250	2 AYV5321
5	47	100.0	325	3 AYV5324
6	44	93.6	329	3 AYV5328
7	44	93.6	329	3 AYV5325
8	44	93.6	329	5 AAO17334
9	44	93.6	329	5 AAO17334
10	44	93.6	332	2 AAY1079
11	41	87.2	280	2 AAY1078
12	41	87.2	329	2 AAY1076
13	38	80.9	303	4 AAU0963
14	38	80.9	303	6 ABM7482
15	37	78.7	103	7 ABO79371
16	36	76.6	261	5 ABM8788
17	36	76.6	261	6 ABU3032
18	35	74.5	252	2 AYU33916
19	34	72.3	38	4 AAM21828
20	34	72.3	38	4 ABB44199
21	34	72.3	38	4 AAM8152
22	34	72.3	38	4 ABB27077
23	34	72.3	38	4 AAM7933
24	34	72.3	38	4 AAM6230
25	34	72.3	38	4 ABG59572

Key	Location/Qualifiers
FT	1..17
Peptide	/note= "OVA323-339"
FT	18..26
FT	/note= "B7-2 amino acids 113-121"
XX	
XX	W020037102-A2.
XX	29-JUN-2000.
XX	DD
XX	17-DEC-1999;
PF	99W0-GB004200.
XX	PR
PR	19-DEC-1998;
PR	99GB-00027921.
PR	23-OCT-1999;
PR	99GB-00025015.
XX	(MLML-1) ML LAB PLC.
PA	
XX	Lechner RI, Rogers NJ, Dorling A;
XX	WPI; 2000-442537/38.
XX	
XX	Novel methods for improving tolerance to a xenograft comprising immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX	Disclosure; Page 23; 81pp; English.
CC	The present sequence is that of chimeric peptide 4 comprising T-cell epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell epitope comprising amino acids 113-121 of pig co-stimulatory molecule

Abg46955 Human pep  
Abg5384 Human pro  
Abg09140 Thermocoll  
Abg97746 T. mariti  
Abu3605 Protein e  
Abb92863 Herbicida  
Abb94369 Human pro  
Abg8525 Adenyl cy  
Ari9251 Murine ad  
Ari9521 Human pol  
Aam41307 Human pol  
Akk4934 Novel hum  
Ari58345 XW\_031992  
Abd63241 Human bre  
Adj68477 Human hea  
Adj66594 Rf5 prot  
Aam78839 Human pro  
Aam79823 Human pro  
Abg5831 BCR0518 P  
Add18610 Human dis

#### ALIGNMENTS

CC CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for CC inhibiting costimulation by porcine cells of human T cells, with CC particular importance in the context of xenotransplantation of porcine CC organs. Recipients are immunised with hybrid synthetic peptides, such as CC the present peptide, comprising a T cell epitope conjugated to sequences CC of the porcine costimulatory molecule CD80, CD86 or CD40. Peptides that CC induce antibodies specific for regions of costimulatory molecules CC involved in binding to their counter-receptors on human cells are capable CC of blocking the delivery of costimulation. Once the antibody response has CC been induced, the transplanted organ will recall this response due to the CC expression of the costimulatory molecules, thereby sustaining the CC blockade. The method is useful for improving the tolerance of a host to CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12- CC SEP-2003 to standardise OS field)

Sequence 26 AA;

Query Match 100.0%; Score 47; DB 3; length 26;  
Best Local Similarity 100.0%; Pred. No. 0.012; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLVPIHOMS 9  
Dp 18 GLVPIHOMS 26

RESULT 2

ID AAY95327  
XX AAY95327 standard; peptide; 30 AA.

XX AAY95327;  
AC AAY95327;  
DT 12-SEP-2003 (revised)  
DT 25-SEP-2000 (first entry)

DB OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 3.  
XX KW Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;  
KW xenotransplantation; organ transplant; vaccine; B-cell epitope;  
T-cell epitope; ovalbumin; chicken.  
XX OS Callus sp.  
OS Sus scrofa.  
OS Chimeric.

XX FH Key Location/Qualifiers  
PT peptide 1..17  
PT /note= "OVA323-339"  
PT Peptide 18..30  
PT /note= "B7-2 amino acids 109-121"

XX PN WO20037102-A2.  
XX PD 29-JUN-2000.

XX PR 17-DEC-1999; 99WO-GB004200.

XX PR 19-DEC-1998; 99GB-00027921.  
XX PR 23-OCT-1999; 99GB-00025015.

DA (MML-) ML LAB PLC.

XX PI Lechner RI, Rogers NJ, Dorling A;  
XX WPI; 2000-442537/38.

XX PT Novel methods for improving tolerance to a xenograft comprising  
PT immunizing a mammal with a T-cell epitope and a B-cell epitope.  
XX Disclosure; Page 23; 81pp; English.

CC The present sequence is that of chimeric peptide 3 comprising T-cell  
CC Sequence 26 AA;

Query Match 100.0%; Score 47; DB 3; length 30;  
Best Local Similarity 100.0%; Pred. No. 0.015; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLVPIHOMS 9  
Dp 22 GLVPIHOMS 30

RESULT 3

ID AAW14944  
XX AAW14944 standard; protein; 250 AA.

XX AAW14944;  
DT 17-OCT-2003 (revised)  
DT 16-JUN-1997 (first entry)

DE Chimeric human/porcine CD86.  
XX KW Xenotransplantation; graft rejection; cell interaction; pig; CD88;  
KW monoclonal antibody; chimeric antibody; diagnosis.  
XX OS Homo; sapiens.  
OS Sus scrofa.  
OS Chimeric.

XX FH Key Location/Qualifiers  
PT Peptide 1..25  
PT /label= Sig\_peptide  
PT Protein 26..250  
PT /label= Mat\_Protein  
PT Region 246..250  
PT /label= Histidine\_tag

XX PN WO9711971-A1.

XX PR 03-APR-1997.

XX PF 27-SEP-1996; 96WO-US015575.

XX PR 28-SEP-1995; 95US-000489P.

XX PR 26-SEP-1996; 96US-0004489.

XX PA (ALEX-) ALEXION PHARM INC.

XX PT Mueller JP, Evans MJ, Mueller EB, Rollins S, Rother RP, Matis LA;

XX DR WPI; 1997-212855-19.

XX DR N-FSDB; AAT62939.

CC Antibodies binding to porcine but not human cell interaction proteins -  
CC useful to treat and assay for rejection of xenografted porcine organs -

PT tissues or cells.

PI Lechler RI, Rogers NJ, Dorling A;

XX XX XX DR WPI; 2000-442537/38.

PS Disclosure; Page 69-70; 105pp; English.

XX XX XX DR N-PSDB; AAA4961.

CC A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino acid residues 1-4 and 197-245 from human CD86, and amino acids 5-196 from porcine CD86. It is encoded by a DNA construct (AAV62939) obt'd. by PCR amplification of porcine sequences and ligation to a sequence encoding the C-terminal region of human CD86 IGC domain. A signal sequence facilitates efficient secretion from transfected mammalian cells.

CC Antibodies to porcine CD86 protein, P-selectin (see also AAV14945) and vascular cell adhesion molecule (see also AAV14931-4) are useful for diagnosing human rejection or porcine xenotransplants and/or improving xenotransplantation of porcine cells, tissues and organs into human recipients. (updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 250 AA;

Query Match 100.0%; Score 47; DB 2; Length 250; Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9

Db 119 GLVPIHQMS 127

RESULT 4

AY95321 ID AAY95321 standard; protein; 325 AA.

XX XX AC AAY95321;

XX DT 25-SEP-2000 (first entry)

XX D3 pig costimulatory molecule CD86 (B7-2).

XX KW Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;

XX KW xerotransplantation; organ transplant; vaccine; epitope.

OS Sus scrofa.

XX Key Location/Qualifiers

FH Peptide 17..29

FT Peptide /note= "peptide 9"

FT Peptide 21..32

FT Peptide /note= "peptide 8"

FT Peptide 32..40

FT Peptide /note= "peptide 2"

FT Peptide 76..88

FT Peptide /note= "peptide 10"

FT Peptide 81..90

FT Peptide /note= "peptide 1"

FT Peptide 94..104

FT Peptide /note= "peptide 5"

FT Peptide 109..121

FT Peptide /note= "peptide 3"

FT Peptide 113..121

FT Peptide /note= "peptide 4"

FT Peptide 151..162

FT Peptide /note= "peptide 6"

XX WO20037102-A2.

XX PD 29-JUN-2000.

XX PF 17-DEC-1999; 99WO-GB004200.

XX PR 19-DEC-1998; 98GB-00027921.

XX PR 23-OCT-1999; 99GB-00025015.

XX PA (MLML -) ML LAB PLC.

PI Lechler RI, Rogers NJ, Dorling A;

XX XX XX DR WPI; 2000-442537/38.

PS Disclosure; Fig 6; 81pp; English.

CC The present sequence is that of pig co-stimulatory molecule CD86 (B7-2), as deduced from an isolated cDNA clone (see AAV49661). CD86 plays a key role in T cell costimulation. The invention relates to a novel strategy for inhibiting costimulation by porcine cells of human T cells, with particular importance in the context of xerotransplantation of porcine organs. Recipients are immunised with hybrid synthetic peptides comprising a T cell epitope conjugated to sequences of the porcine co-stimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86 (see also AAV95325-33). Peptides that induce antibodies specific for receptors on human cells (CD86 and CD14) are capable of blocking the delivery of costimulation. Once the antibody response has been induced, the transplanted organ will recall this response due to the expression of the costimulatory molecules, thereby sustaining the response, and providing an endogenous mechanism of costimulatory blockade. The method is useful for improving the tolerance of a host to xenografts, particularly porcine pancreatic islet cells

XX SQ Sequence 325 AA;

AY95324 ID AAY95324 standard; protein; 325 AA.

XX XX AC AAY95324;

XX DT 25-SEP-2000 (first entry)

XX DE Human costimulatory molecule CD86 (B7-2).

XX KW Co-stimulatory molecule; CD86; B7-2; human; immunosuppressive;

XX KW xerotransplantation; organ transplant; vaccine; epitope.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Peptide 19..42

FT Peptide /note= "epitope"

FT Peptide 53..73

FT Peptide /note= "epitope"

FT Peptide 101..129

FT Peptide /note= "epitope"

FT Peptide 156..165

FT Peptide /note= "epitope"

XX PN WO20037102-A2.

XX PD 29-JUN-2000.

XX PF 17-DEC-1999; 99WO-GB004200.

XX PR 19-DEC-1998; 98GB-00027921.

XX PR 23-OCT-1999; 99GB-00025015.

XX PA

(MLML-) ML LAB PLC.  
 XX  
 PT Lechler RI, Rogers NJ, Dorling A;  
 XX  
 DR WPI; 2000-442537/38.  
 XX  
 PT Novel methods for improving tolerance to a xenocraft comprising  
 PT immunizing a mammal with a T-cell epitope and a B-cell epitope.  
 XX  
 PG Disclosure; Fig 26; 81PP; English.  
 XX  
 The present sequence is that of human co-stimulatory molecule CD86 (B7-2). CD86 plays a key role in T cell costimulation. The invention relates to a novel strategy for inhibiting costimulation by porcine cells of human T cells, with particular importance in the context of xenotransplantation of porcine organs. Recipients are immunised with hybrid synthetic peptides comprising a T cell epitope conjugated to sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see ALY9522-24). Peptides that induce antibodies specific for regions of costimulatory molecules involved in binding to their counter-receptors on human cells (CD28 and CD4) are capable of blocking the delivery of costimulation. Once the antibody response has been induced, the transplanted organ will recall this response due to the expression of the costimulatory molecules, thereby sustaining the response, and providing an endogenous mechanism of costimulation blockade. The method is useful for improving the tolerance of a host to xenografts, particularly Porcine pancreatic islet cells  
 XX  
 Sequence 325 AA;

Query Match 100.0%; Score 47; DB 3; Length 325;

Best Local Similarity 100.0%; Pred. No. 0.23; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GLVPIHOMS 9  
 Db 113 GLVPIHOMS 121

RESULT 6  
 AAY32278  
 ID AAY32278 standard; protein; 329 AA.  
 XX  
 AC AAY32278;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 15-FEB-2000 (first entry)  
 DE Cat CB86 (B7-2) ligand.

XX  
 CD86: B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;

XX  
 feline leukaemia virus; feline infectious peritonitis virus; FIPV;  
 XX  
 feline panleukopenia virus; feline calicivirus; feline reovirus-3;  
 XX  
 feline rotavirus; feline coronavirus; feline syncytial virus;  
 XX  
 feline sarcoma virus; feline herpesvirus; feline Borna disease;  
 XX  
 rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis; Dirofilaria immitis; or a flea; bacterial pathogen; or parasite (all claimed);  
 XX  
 parasite; autoimmune disease; transplant rejection; therapy;  
 XX  
 feline calicivirus; feline rotavirus; feline coronavirus; feline syncytial virus; feline leukaemia virus; feline infectious peritonitis virus; FIPV; feline panleukopenia virus; feline calicivirus; feline reovirus-3; feline rotavirus; feline coronavirus; feline syncytial virus; feline sarcoma virus; feline herpesvirus; feline Borna disease; rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis; Dirofilaria immitis; or a flea; bacterial pathogen; or parasite (all claimed);  
 XX  
 Felis catus.

OS Felis catus.

XX  
 PN WO9957271-A2.

PD 11-NOV-1999.  
 XX  
 30-APR-1999; 99WO-US009502.

XX  
 PR 01-MAY-1998; 98US-00071699.

PA (TEXAS ) TEXAS A & M SYSTEM.  
 XX  
 PI Collision EW, Hash SM, Choi I;

XX  
 WPI; 2000-052972/04.

DR N-PSDB; AA234785.  
 XX  
 Novel feline proteins used to produce feline vaccines which prevent PT  
 PT  
 infectious disease or to promote growth in homologous or heterologous species.  
 XX  
 PS Example 1A; Fig 3A; 186PP; English.  
 XX  
 The present sequence represents feline CD86 (B7-2) ligand, as predicted from isolated cDNA of peripheral blood mononuclear cells. The coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279) and a tumour antigen or an antigen from a pathogenic organism has the ability to activate or enhance activation of T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation of T-lymphocytes. The invention provides isolated nucleic acids encoding feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic acids, and polypeptides encoded by the nucleic acids. It also provides vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and further comprising immunogens derived from pathogens, especially feline immunodeficiency virus (FIV), feline leukaemia virus, feline infectious feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial virus, feline sarcoma virus, feline herpesvirus, feline Borna disease virus, rabies virus, chlamydia; Toxoplasmosis gondii; Dirofilaria immitis, or a flea; bacterial pathogen, or parasite (all claimed).  
 CC Vaccines capable of enhancing an immune response, and vaccines capable of suppressing an immune response (suitable for treating an autoimmune disease or tissue or organ transplant rejection) are claimed. (Updated on 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 329 AA;

Query Match 93.6%; Score 44; DB 3; Length 329;

Best Local Similarity 88.9%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GLVPIHOMS 9  
 Db 120 GLVPMHQMS 128

RESULT 7  
 AAY32285  
 ID AAY32285 standard; protein; 329 AA.  
 XX  
 AC AAY32285;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 28-FEB-2000 (first entry)  
 DE Feline CD86 (B7-2).

XX  
 CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator; tumour; cancer; therapy.  
 XX  
 Felis catus.

OS WO9957295-A1.  
 XX  
 PN 11-NOV-1999.  
 XX  
 30-APR-1999; 99WO-US009504.

XX  
 PR 01-MAY-1998; 98US-00071711.

XX  
 PA (SCHIE ) SCHERING-PLOUGH LTD.

PA (SCHIE ) SCHERING-PLOUGH VETERINARY CORP.  
 XX  
 PI Winslow BJ, Cochran MD;

XX  
 DR WPI; 2000-062155/05.

DR N-PSDB; AA234838.

XX Novel recombinant virus useful as immunomodulators, particularly in  
 PT vaccines.  
 XX Disclosure; Fig 3A; 230pp; English.

PS This sequence represents feline CD86 (B7-2), as deduced from peripheral  
 PT blood mononuclear cell cDNA (see AAK24938). Manipulating the expression  
 XX of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)  
 CC relates to a recombinant virus that contains at least one foreign nucleic  
 CC acid, inserted into a non-sensitising genomic region, that encodes feline  
 CC CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and  
 CC is expressed when the recombinant virus is introduced into a suitable  
 CC host. The invention also provides: a recombinant virus further comprising  
 CC a foreign nucleic acid encoding an immunogen derived from a feline  
 CC pathogen; recombinant viruses capable of enhancing an immune response to  
 CC protect against disease; recombinant viruses expressing antisense  
 CC sequences, capable of suppressing an immune response in a feline, e.g.,  
 CC for treatment of autoimmune disease or transplant rejection; and  
 CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used to  
 CC reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to  
 CC standardise OS field)

XX Sequence 329 AA;

SQ Query Match 93.6%; Score 44; DB 3; Length 329;  
 Best Local Similarity 88.9%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHOMS 9  
 Db 120 GLVPIHOMS 128

RESULT 8  
 AA017734 standard; protein; 329 AA.  
 ID AA017734  
 XX AC AC017734;  
 XX DT 08-AUG-2002 (first entry)  
 DE Feline CD86.  
 XX  
 KW Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;  
 KW feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;  
 KW CTLA-4; vaccine; rabies; autoimmune disease; organ transplant;  
 KW toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukaemia;  
 KW FeLV; calcivirus; rotavirus; reovirus type 3; coronavirus; herpes;  
 KW feline disease.  
 XX  
 OS Felis sp.  
 XX  
 PN US2002028208-A1.  
 XX PD 07-MAR-2002.  
 XX  
 PR 30-APR-1999; 99US-00303510.  
 PR 01-MAY-1998; 98US-0083869P.  
 XX  
 PA (COLL/1) COLLISON E W.  
 PA (HASH/1) HASH S M.  
 PA (CHOI/1) CHOI I.  
 XX  
 PI Collison EW, Hash SM, Choi I;  
 XX  
 DR WPI; 2002-315045/35.  
 DR N-PSDB; A8K48230.

XX This invention relates to the DNA and protein sequences encoding a  
 DR N-PSDB; A8K4840.  
 XX  
 PT New recombinant virus, useful for immunizing felines to prevent or treat  
 PT feline immunodeficiency virus, comprises foreign nucleic acid encoding  
 PT feline immunodeficiency virus, comprising an effective amount of these  
 PT receptor proteins. A vaccine is useful for inducing immunity or enhancing  
 PT feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or  
 XX CTLA-4. The protein sequences of the invention are useful for suppressing an immune response in a feline suffering from an

PS Disclosure; Fig 3; 77pp; English.

XX The present invention relates to a recombinant virus comprising at least  
 CC one foreign nucleic acid encoding a protein selected from feline  
 CC cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,  
 CC which is capable of expression when the virus is introduced into an  
 CC appropriate host. The virus can be administered to the feline in order to  
 CC elicit or enhance an immune response to prevent or treat feline  
 CC immunodeficiency disease, feline leukaemia, feline infectious peritonitis,  
 CC cancers, degenerative and autoimmune diseases and immunodeficiency. The  
 CC present sequence is a cytotoxic T lymphocyte accessory molecule described  
 XX in the exemplification of the invention

SQ Sequence 329 AA;

Query Match 93.6%; Score 44; DB 5; Length 329;  
 Best Local Similarity 88.9%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9  
 Db 120 GLVPIHOMS 128

RESULT 9  
 AAUT8121  
 ID AAUT8121 standard; protein; 329 AA.  
 XX AC AAUT8121;  
 XX DT 02-JUL-2002 (first entry)  
 DE Feline CD86 protein.  
 XX  
 KW Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;  
 KW feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;  
 KW CTLA-4; vaccine; rabies; autoimmune disease; organ transplant;  
 KW toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukaemia;  
 KW FeLV; calcivirus; rotavirus; reovirus type 3; coronavirus; herpes;  
 KW feline disease.  
 XX  
 OS Felis sp.  
 XX  
 PN US2002028208-A1.  
 XX PD 07-MAR-2002.  
 XX  
 PR 30-APR-1999; 99US-00303510.  
 PR 01-MAY-1998; 98US-0083869P.  
 XX  
 PA (COLL/1) COLLISON E W.  
 PA (HASH/1) HASH S M.  
 PA (CHOI/1) CHOI I.  
 XX  
 PI Collison EW, Hash SM, Choi I;  
 XX  
 DR WPI; 2002-315045/35.  
 DR N-PSDB; A8K48230.

XX This invention relates to the DNA and protein sequences encoding a  
 DR N-PSDB; A8K4840.  
 XX  
 PT Polynucleotide encoding Polypeptide of CD80 ligand, CD86 ligand, CD28  
 PT receptor or CTLA-4 receptor as vaccine for inducing immune response in  
 PT feline suffering from autoimmune disease or tissue or organ transplant.  
 XX  
 PS Disclosure; Fig 3A; 73pp; English.  
 XX  
 CC This invention relates to the DNA and protein sequences encoding a  
 CC soluble CD80 ligand, soluble CD86 ligand, soluble and membrane-bound CD28  
 CC receptor and soluble or membrane bound CTLA-4 receptor. The invention  
 CC also relates to a vaccine comprising an effective amount of these  
 CC receptor proteins. A vaccine is useful for inducing immunity or enhancing  
 CC immune response in a cat. The protein sequences of the invention are  
 CC useful for suppressing an immune response in a feline suffering from an

CC autoimmune disease or the recipient of a tissue or organ transplant. A  
 CC vector containing the DNA sequences of the invention is useful for  
 CC redirecting an immune response in a feline to an immunogen such as rabies  
 CC virus, chlamydia, toxoplasmosis gondii, flea, feline immunodeficiency  
 CC virus, feline leukaemia (fELV), feline infectious peritonitis virus  
 CC (FIP), panleukopenia virus, calicivirus, reovirus type 3, rotavirus,  
 CC coronavirus, syncytial virus, herpes virus, sarcoma virus, bovine disease  
 CC virus or a parasite. The protein sequences may be further utilised to  
 CC promote growth in homologous or heterologous feline species. Enhancement  
 CC of immunity through the interaction of soluble CD80 or soluble CD86 with  
 CC CD28 or CTLA-4 or inhibition of an immune response through the  
 CC interaction of feline CD80 or CD86 with CTLA-4 takes advantage of the  
 CC natural process of regulation rather than adding foreign substances that  
 CC could have multiple, even detrimental effects on overall or long term  
 CC health. The present sequence represents feline CD86 protein of the  
 CC invention

SQ Sequence 329 AA;

Qy	1 GLYPRHQMS 9	120 GLVPMHQMS 128
Query	AY41079	
Match	93.6%	Score 44; DB 5; Length 329;
Best Local Similarity	88.9%	Pred. No. 1; Mismatches 0; Indels 0; Gaps 0
Matches	8;	Conservative 1; Mismatches 0; Indels 0; Gaps 0
Db		

RESULT 10

ID	AY41079 standard; protein; 332 AA.
XX	
AC	AY41079;
XX	
DT	20-DEC-1999 (first entry)
XX	
DB	Feline B7-2 protein.
XX	
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW	allergic reaction; infectious disease; tumor development; feline;
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX	
OS	Felis catus.
XX	
PN	WO9947558-A2.
XX	
PD	23-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US0005187.
XX	
PR	19-MAR-1998; 98US-0078165P.
PR	17-APR-1998; 98US-00062597.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Sellins KS;
XX	
DR	WPI; 1999-571822/48.
XX	
PT	N-PSDB; AAZ227929, AAZ227931.
XX	
PT	New isolated B7 and CTLA nucleic acids, used to develop products for XX treating, e.g. autoimmune and atopic diseases.
PS	Claim 4; Page 116-119; 148pp; English.
XX	
CC	The invention provides B7 and CTLA (T cell costimulatory proteins) CC encoding nucleic acid molecules from dogs and cats. The proteins can be CC expressed by standard recombinant methodology. The nucleic acid molecules CC and the encoded proteins can be used for preventing or treating diseases, CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor CC development, graft rejection, inflammation, arthritic and atopic diseases, CC such as atopic dermatitis. They can be used in mammals such as humans, dogs, CC cats, cattle, sheep or pets. The products can also be used for detection,

Sequence	332 AA;	diagnosis and drug screening
XX	XX	Query Match: 93.6%; Score 44; DB 2; length 332;
CC	CC	Best Local Similarity 88.9%; Prec. No. 1; Mismatches 8;
CC	CC	Matches 1; Conservative 1; MisMatches 0; Indels 0; Gaps 0;
SQ	SQ	QY 1 GLVPHQMS 9
		DB 120 GLVPHQMS 128
		RESULT 11.
		RAY41078
		ID AAY41078 Standard; protein; 280 AA.
		AC AAY41078;
		XX
		DT 20-DEC-1999 (first entry)
		XX
		DB Canine B7-2S Protein.
		XX
		KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine;
		KW graft rejection; inflammation; arthritis; atopic dermatitis.
		XX
		OS Canis familiaris.
		XX
		PN W09947558-A2.
		XX
		PD 23-SEP-1999.
		XX
		PF 19-MAR-1999; 99W0-US006187.
		XX
		PR 19-MAR-1998; 98US-0078765P.
		PR 17-APR-1998; 98US-00062597.
		XX
		PA (HESK-) HESKA CORP.
		XX
		PI Sim G, Yang S, Sellins KS;
		XX
		DR WPI; 1999-571822/48.
		XX
		DR N-PSSDB; AAZ27921, AAZ27923.
		PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
		PT treating, e.g. autoimmune and atopic diseases.
		XX
		PS Claim 4; Page 109-111; 148PP; English.
		XX
		The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such as humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.
		Sequence 280 AA;

ID AAY41076 standard; protein; 329 AA.  
 XX  
 AC AAY41076;  
 XX  
 DT 20-DEC-1999 (first entry)  
 XX  
 DE Canine B7-2 protein.  
 XX  
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO9947558-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 99WO-US006187.  
 XX  
 PR 19-MAR-1999; 98US-0078765P.  
 PR 17-APR-1998; 98US-00062597.  
 PR (HESK-1) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Sellins KS;  
 XX  
 DR WPI; 1999-57182/48;  
 XX  
 N-PSDB; A2227913, A2227915.  
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases.  
 XX  
 PS Claim 4; Page 97-99; 1483P; English.  
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such as humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.  
 XX  
 SQ Sequence 329 AA;  
 Query Match 87.2%; Score 41; DB 2; Length 329;  
 Best Local Similarity 77.8%; Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GLYPIHQS 9  
 Db 119 GLYPMHQDN 127  
 RESULT 13  
 AAU40963 standard; protein; 303 AA.  
 XX  
 AC AAU40963;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DB Propionibacterium acnes immunogenic protein #1859.  
 XX  
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO2003033515-A1.  
 XX

PN WO200181581-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 20-APR-2001; 2001WO-US012865.  
 XX  
 PR 21-APR-2000; 2000US-0193047P.  
 PR 03-JUN-2000; 2000US-0208841P.  
 PR 07-JUL-2000; 2000US-0216747P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 XX  
 DR WPI; 2001-616774/71.  
 XX  
 N-PSDB; A2359513.  
 PT Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.  
 XX  
 PS Example 1; SEQ ID NO 2158; 1069P; English.  
 XX  
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include Sarcoid syndrome (synovitis), acne, pustulosis, hypersensitivity and osteomyelitis), urethritis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct\\_sequences](http://ftp.wipo.int/pub/published/pct_sequences)  
 XX  
 SQ Sequence 303 AA;  
 Query Match 80.9%; Score 38; DB 4; Length 303;  
 Best Local Similarity 66.7%; Pred. No. 17; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 GLYPIHQS 9  
 Db 35 GIAPIHQS 43  
 RESULT 14  
 ABM37482 standard; protein; 303 AA.  
 XX  
 AC ABM37482;  
 XX  
 DT 20-OCT-2003 (first entry)  
 XX  
 DB Propionibacterium acnes predicted ORF-encoded polypeptide #2158.  
 XX  
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial; immunostimulant; immune response; vaccine.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO2003033515-A1.  
 XX

PD  
XX  
PP  
11-OCT-2002; 2002WO-US032727.  
PR  
XX  
15-OCT-2001; 2001US-00978825.  
XX  
PA  
XX  
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JT;  
PI Zhang Y, Wang S, Jen S,洛德斯 MJ, Benson DR, Jones R, Carter D;  
PI Barth B, Vallieve-Douglas J;  
XX  
DR  
DR  
WPI; 2003-381789/36.  
N-PADB; ACP64442.  
XX  
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the  
polypeptide, useful for diagnosing, preventing or treating acne vulgaris.  
PT or for stimulating an immune response specific for a *P. acnes* protein.  
XX  
PS Example 1; SEQ ID NO 2158; 1481PP; English.  
XX  
CC The invention relates to an isolated polynucleotide (ACP64435-ACP64731)  
CC encoding a Propionibacterium acnes protein. The invention also relates to  
CC polypeptides encoded by the polynucleotides (ABM3624-ABM6336) and to  
CC immunogenic fragments of *P. acnes* polypeptides. The invention  
CC additionally encompasses expression vector and host cells comprising a  
CC polynucleotide of the invention; antibodies against polypeptides of the  
CC invention; fusion proteins comprising a polypeptide of the invention; a  
CC method for stimulating an immune response specific for a *P. acnes*  
CC polypeptide and an isolated T cell population comprising T cells prepared  
via this method; a vaccine composition (comprising *P. acnes* polypeptides  
CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
CC antigen-presenting cells that express the polypeptide); a method and kit  
CC for detecting or determining the presence or absence of *P. acnes* in a  
CC patient; and a method for inhibiting the development of *P. acnes* in a  
CC patient. The *P. acnes* polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations or antigen-presenting cells that express the  
CC *vulgaris*, or for stimulating an immune response specific for a *P. acnes*  
CC protein. The polynucleotides can also be used as probes or primers for  
CC nucleic acid hybridization. The vaccine composition is useful for the  
CC stimulation of an immune response against *P. acnes*, or for treating acne  
CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence relates to a polypeptide predicted to be encoded by an ORF (open  
CC reading frame) contained within the *P. acnes* polynucleotides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
SQ Sequence 303 AA:  
Query Match 80.9%; Score 38; DB 6; Length 303;  
Best Local Similarity 66.3%; Pred. No. 17; Matches 6;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0  
OY 1 GLVPIHQMS 9  
|:||:||:  
Db 35 GIAPIHOLS 43  
RESULT 15  
AB079571  
ID AB079571 standard; protein; 103 AA.  
XX  
AC AB079571;  
XX  
DT 29-JUL-2004 (First entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #11746.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.

(GENO-) GENOME THERAPEUTICS CORP.  
Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
WPI: 2003-6151309/5B.  
N-PSDB; ADD1342.

**Disclosure:** SEQ ID NO 28317: 4552P; English.

The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences ABO67826-ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

Sequence 103 AA;

CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence represents a polypeptide predicted to be encoded by an OR [open  
CC reading frame] contained within the *P. acnes* polyribonucleotides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX

SQ

Sequence 303 AA;



PRIOR FILING DATE: 1999-12-21  
 PRIOR APPLICATION NUMBER: 60/183578  
 PRIORITY: US-09-651-200-18  
 PRIORITY NUMBER: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 18  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: *Felis catus*  
 US-09-651-200-18

Query Match 93.6%; Score 44; DB 4; Length 329;  
 Best Local Similarity 88.9%; Pred. No. 0.22; 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9  
 ||||:|||:  
 Db 120 GLVPMHQMS 128

RESULT 3  
 US-09-303-040-6  
 Sequence 6, Application US/09303040  
 Patent No. 655175  
 GENERAL INFORMATION:  
 APPLICANT: Winslow, Barbara J.  
 TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding  
 TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or  
 TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof  
 FILE REFERENCE: 54957-B

CURRENT APPLICATION NUMBER: US/09/303,040  
 CURRENT FILING DATE: 1999-04-30  
 EARLIER APPLICATION NUMBER: 60/083,870  
 EARLIER FILING DATE: 1998-05-01  
 NUMBER OF SEQ ID NOS: 82  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 6  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: *feline* CDB6  
 US-09-303-040-6

Query Match 93.6%; Score 44; DB 4; Length 329;  
 Best Local Similarity 88.9%; Pred. No. 0.22; 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9  
 ||||:|||:  
 Db 120 GLVPMHQMS 128

RESULT 4  
 US-09-651-200-19  
 Sequence 19, Application US/09651200  
 Patent No. 5429303  
 GENERAL INFORMATION:  
 APPLICANT: Green et al.  
 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 TITLE OF INVENTION: Polypeptides Encoded Thereby  
 FILE REFERENCE: 15966-562 (CURA-62)  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 CURRENT FILING DATE: 2000-02-18  
 PRIOR APPLICATION NUMBER: 60/152383  
 PRIOR FILING DATE: 1999-09-03  
 PRIOR APPLICATION NUMBER: 60/173909  
 PRIOR FILING DATE: 1999-12-21  
 PRIOR APPLICATION NUMBER: 60/183578  
 PRIOR FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 19

Query Match 72.3%; Score 34; DB 3; Length 1305;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+02; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9  
 ||||:|||:  
 Db 1249 GVVPHQMS 1257

RESULT 5  
 US-09-252-991A-28317  
 Sequence 28317, Application US/09252991A  
 Patent No. 655175  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 107196,136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-01-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO: 28317  
 LENGTH: 103  
 TYPE: PRT  
 ORGANISM: *Pseudomonas aeruginosa*  
 US-09-252-991A-28317

Query Match 78.7%; Score 37; DB 4; Length 103;  
 Best Local Similarity 66.7%; Pred. No. 1.8; 2; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9  
 ||||:|||:  
 Db 61 GLTPPIHQLA 69

RESULT 6  
 US-08-864-785-3  
 Sequence 3, Application US/08864785A  
 Patent No. 632956  
 GENERAL INFORMATION:  
 APPLICANT: Kaplan, Joshua M.  
 APPLICANT: Oppenheimer, Allison J.  
 APPLICANT: Hartz, Anne C.  
 TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,  
 TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION  
 CURRENT APPLICATION NUMBER: US/08/864,785A  
 CURRENT FILING DATE: 1997-05-29  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 3  
 LENGTH: 1305  
 TYPE: PRT  
 ORGANISM: *Mus musculus*  
 US-08-864-785-3

Query Match 72.3%; Score 34; DB 3; Length 1305;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+02; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9  
 ||||:|||:  
 Db 1249 GVVPHQMS 1257

RESULT 7  
US-08-894-173-2  
Sequence 2, Application US/08894173A  
; Patent No. 609612  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Adenylate cyclase and uses therefor  
; FILE REFERENCE: P1716C  
; CURRENT APPLICATION NUMBER: US/08/894,173A  
; CURRENT FILING DATE: 1997-08-13  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1353  
; TYPE: PRT  
; ORGANISM: Mouse  
; FEATURE:  
; OTHER INFORMATION: HYPOTHETICAL : NO

US-08-894-173-2

Query Match Similarity 72.3%; Score 34; DB 3; Length 1353;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQMS 9  
Db 1249 GVVPOHQLS 1257

RESULT 8  
US-09-398-193-2  
Sequence 2, Application US/09398193  
; Patent No. 6177581  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Adenylylate cyclase and uses therefor  
; FILE REFERENCE: P24360-  
; CURRENT APPLICATION NUMBER: US/09/398,193  
; CURRENT FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1353  
; TYPE: PRT  
; ORGANISM: Mouse  
; FEATURE:  
; OTHER INFORMATION: HYPOTHETICAL : NO

US-09-398-193-2

Query Match Similarity 72.3%; Score 34; DB 3; Length 1353;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQMS 9  
Db 1249 GVVPOHQLS 1257

RESULT 9  
US-09-473-717-3  
Sequence 3, Application US/09473717  
; Patent No. 6372475  
; GENERAL INFORMATION:  
; APPLICANT: Storm, Daniel R.  
; APPLICANT: Hacker, Beth  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Cor Therapeutics, Inc.  
; APPLICANT: University of Washington  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE REFERENCE: 44481-5029-01-US

RESULT 9  
US-09-473-717-3  
Sequence 3, Application US/09473717  
; Patent No. 6372475  
; GENERAL INFORMATION:  
; APPLICANT: Storm, Daniel R.  
; APPLICANT: Hacker, Beth  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: Cor Therapeutics, Inc.  
; APPLICANT: University of Washington  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE REFERENCE: 44481-5029-01-US

RESULT 10  
US-09-538-092-1329  
Sequence 1329, Application US/09538092  
; Patent No. 6753114  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 1596-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuraPatSeqFormatter Version 0.9  
; SEQ ID NO 1329  
; LENGTH: 1884  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)..(0)  
; OTHER INFORMATION: PolyPeptide Accession Number Q14690

US-09-538-092-1329

Query Match Similarity 72.3%; Score 34; DB 3; Length 1353;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQMS 9  
Db 1249 GVVPOHQLS 1257

RESULT 11  
US-09-270-767-44136  
Sequence 44136, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Hamburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7726-034  
; CURRENT APPLICATION NUMBER: US/09/270,167  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 6517  
; SOFTWARE: Patentin Ver. 2.0

```

; SEQ ID NO: 44136
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-44136

Query Match 70.2%; Score 33; DB 4; Length 249;
Best Local Similarity 75.0%; Pred. No. 35; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 LVPHQMS 9
Db 7 MVIPIHMS 14

RESULT 12
; Sequence 3290, Application US/09134001C
; Patent No: 6380370
; GENERAL INFORMATION:
; APPLICANT: Lytin Boucette-Stramm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: 575C-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 3290
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-3290

Query Match 70.2%; Score 33; DB 3; Length 275;
Best Local Similarity 71.4%; Pred. No. 39; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 3 VPIHQMS 9
Db 159 VPVHQLS 165

RESULT 13
; Sequence 3134, Application US/09252991A
; Patent No: 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 3314
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-31314

Query Match 70.2%; Score 33; DB 3; Length 275;
Best Local Similarity 71.4%; Pred. No. 39; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 3 VPIHQMS 9
Db 159 VPVHQLS 165

RESULT 14
; Sequence 28266, Application US/09252991A
; Patent No: 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 525
; SEQ ID NO: 28266
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-28266

Query Match 70.2%; Score 33; DB 4; Length 525;
Best Local Similarity 55.6%; Pred. No. 83; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GLVPHQMS 9
Db 288 GQVPHQLA 296

RESULT 15
; Sequence 7293, Application US/09621976
; Patent No: 6631903
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET-054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 7293
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-621-976-7293

Query Match 68.1%; Score 32; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 18; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 LVPHQ 7
Db 17 LVPHQ 22

Search completed: December 15, 2004, 16:38:41
Job time : 16.4286 secs

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GENERAL INFORMATION:  
 APPLICANT: Winslow, Barbara J.  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding  
 Current Application Number: US/10/790,396  
 TITLE OF INVENTION: Feline CD80, Feline CD28, Feline CTLA-4 or  
 Current Application Number: US/09/646,561  
 Current Filing Date: 1999-04-30  
 Earlier Application Number: US/09/303,040  
 Earlier Filing Date: 1998-05-01  
 Number of SEQ ID NOS: 82  
 Software: PatentIn Ver. 2.0  
 SEQ ID NO: 6  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: feline CD86  
 US-10-303-040-6

RESULT 3  
 US-10-90-396-26  
 Sequence 26, Application US/10/790396  
 Publication No. US20040157296A1  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Sellins, Karen S.  
 TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
 FILE REFERENCE: IM-1-CI-PCT  
 CURRENT APPLICATION NUMBER: US/10/790,396  
 CURRENT FILING DATE: 2004-03-01  
 PRIOR APPLICATION NUMBER: US/09/646,561  
 PRIOR FILING DATE: 2000-09-19  
 PRIOR APPLICATION NUMBER: 60/078,765  
 PRIOR FILING DATE: 1998-03-19  
 PRIOR APPLICATION NUMBER: 09/062,597  
 PRIOR FILING DATE: 1998-04-17  
 NUMBER OF SEQ ID NOS: 65  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 26  
 LENGTH: 332  
 TYPE: PRT  
 ORGANISM: Felis catus  
 US-10-790-396-26

Query Match 93.6%; Score 44; DB 16; length 332;  
 Best Local Similarity 88.9%; Pred. No. 3.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 120 GLVPMHQMS 128

RESULT 4  
 US-10-790-396-17  
 Sequence 17, Application US/10/790396  
 Publication No. US20040157296A1  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Sellins, Karen S.  
 TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
 FILE REFERENCE: IM-1-CI-PCT  
 CURRENT APPLICATION NUMBER: US/10/790,396  
 CURRENT FILING DATE: 2004-03-01  
 PRIOR APPLICATION NUMBER: US/09/646,561  
 PRIOR FILING DATE: 2000-09-19  
 PRIOR APPLICATION NUMBER: 60/078,765  
 PRIOR FILING DATE: 1998-03-19  
 PRIOR APPLICATION NUMBER: 09/062,597  
 PRIOR FILING DATE: 1998-04-17  
 NUMBER OF SEQ ID NOS: 65  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 26  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: Canis familiaris  
 US-10-790-396-17

Query Match 87.2%; Score 41; DB 16; length 329;  
 Best Local Similarity 77.8%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 119 GLVPMHQMS 127

RESULT 5  
 US-10-790-396-7  
 Sequence 7, Application US/10/790396  
 Publication No. US20040157296A1  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Sellins, Karen S.  
 TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
 FILE REFERENCE: IM-1-CI-PCT  
 CURRENT APPLICATION NUMBER: US/10/790,396  
 CURRENT FILING DATE: 2004-03-01  
 PRIOR APPLICATION NUMBER: US/09/646,561  
 PRIOR FILING DATE: 2000-09-19  
 PRIOR APPLICATION NUMBER: 60/078,765  
 PRIOR FILING DATE: 1998-03-19  
 PRIOR APPLICATION NUMBER: 09/062,597  
 PRIOR FILING DATE: 1998-04-17  
 NUMBER OF SEQ ID NOS: 65  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 7  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: Canis familiaris  
 US-10-790-396-7

Query Match 87.2%; Score 41; DB 16; length 329;  
 Best Local Similarity 77.8%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 119 GLVPMHQMS 127

RESULT 6  
 US-10-425-115-208294  
 Sequence 208294, Application US/10425115  
 Publication No. US2004014272A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants  
 FILE REFERENCE: 38-21(53222)B  
 CURRENT APPLICATION NUMBER: US/10/425,115  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 369326  
 SEQ ID NO: 208294  
 LENGTH: 96  
 TYPE: PRT  
 FEATURE:  
 ORGANISM: Zea mays  
 OTHER INFORMATION: OTHER INFORMATION: Clone ID: MRT4577\_121557C.1.pep  
 US-10-425-115-208294  
 Query Match 78.7%; Score 37; DB 17; Length 96;  
 Best Local Similarity 85.7%; Pred. No. 19;  
 Matches 6; Conservative 1; Mismatches 0;  
 Indels 0; Gaps 0;  
 OY 1 GLVPIHQ 7  
 DB 78 GLVPIHQ 84  
 RESULT 7  
 Sequence 604 Application US/10389647  
 Publication No. US20040033549A1  
 GENERAL INFORMATION:  
 APPLICANT: GREENBERG, E. Peter  
 APPLICANT: SCHUSTER, Martin  
 APPLICANT: LOSROH, Candi  
 TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA  
 FILE REFERENCE: U7Z-038CP  
 CURRENT APPLICATION NUMBER: US10/389,647  
 CURRENT FILING DATE: 2003-03-14  
 PRIOR APPLICATION NUMBER: 09/653730  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 60/153022  
 PRIOR FILING DATE: 1999-09-03  
 NUMBER OF SEQ ID NOS: 710  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 604  
 LENGTH: 99  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-10-389-647-604  
 Query Match 78.7%; Score 37; DB 15; Length 99;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 GLVPIHQMS 9  
 DB 57 GLVPIHQMS 64  
 RESULT 9  
 Sequence 60956 Application US/10282122A  
 Publication No. US20040029129A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Liangu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Olsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.Y.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA-034A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20  
 PRIOR APPLICATION NUMBER: 60/191,078  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/206,848  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 60/207,727  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: 60/230,335  
 PRIOR FILING DATE: 2000-09-06  
 PRIOR APPLICATION NUMBER: 60/230,347  
 PRIOR FILING DATE: 2000-09-09  
 PRIOR APPLICATION NUMBER: 60/242,578  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 60/253,625  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/257,931  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: 60/267,636  
 PRIOR FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: 60/269,308  
 PRIOR FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78614  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 60956  
 TYPE: PRT  
 LENGTH: 261  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 38-21(53222)B  
 CURRENT APPLICATION NUMBER: US/10/425,115  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 369326  
 SEQ ID NO: 321220  
 LENGTH: 122  
 TYPE: PRT  
 OY 1 GLVPIHQMS 9



RESULT 13  
 US-09-935-338-233  
 Sequence 233, Application US/09935338  
 Publication No. US2003C073081A1  
 GENERAL INFORMATION:  
 APPLICANT: MURAI, Hiroyuki  
 APPLICANT: SAGAWA, Hiroaki  
 APPLICANT: UEMORI, Takashi  
 APPLICANT: YAMAMOTO, Junko  
 APPLICANT: TOMONO, Jun  
 APPLICANT: KOBAYASHI, Biji  
 APPLICANT: ENOKI, Tatsushi  
 APPLICANT: TAKEDA, Osamu  
 APPLICANT: MITAKE, Kazue  
 APPLICANT: SATO, Yoshimi  
 APPLICANT: MORIYAMA, Mariko  
 APPLICANT: SAWAGI, Haruhisa  
 APPLICANT: HAGIYA, Michio  
 APPLICANT: ASADA, Kiyoko  
 APPLICANT: KATO, Ikuashin  
 TITLE OF INVENTION: A method for amplification of nucleic acids  
 FILE REFERENCE: MURAI=1  
 CURRENT APPLICATION NUMBER: US/09/935,338  
 CURRENT FILING DATE: 2001-08-23  
 PRIORITY APPLICATION NUMBER: JP2001-076966  
 PRIORITY FILING DATE: 1999-03-19  
 PRIORITY APPLICATION NUMBER: JP11-370035  
 PRIORITY FILING DATE: 1999-12-27  
 PRIORITY APPLICATION NUMBER: JP2000-251981  
 PRIORITY FILING DATE: 2000-08-23  
 PRIORITY APPLICATION NUMBER: JP2000-284419  
 PRIORITY FILING DATE: 2000-09-19  
 PRIORITY APPLICATION NUMBER: JP2000-288750  
 PRIORITY FILING DATE: 2000-09-22  
 PRIORITY APPLICATION NUMBER: JP2001-104191  
 PRIORITY FILING DATE: 2001-04-03  
 PRIORITY APPLICATION NUMBER: PCT/JP00/01534  
 PRIORITY FILING DATE: 2000-03-14  
 NUMBER OF SEQ ID NOS: 290  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 233  
 LENGTH: 238  
 ORGANISM: Thermotoga maritime  
 US-09-935-338-233

Query Match 72.3%; Score 34; DB 15; Length 238;  
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9  
 Db 176 GVLPIHRLS 184

RESULT 15  
 US-10-281-122A-51529  
 Sequence 51529, Application US/10282122A  
 Publication No. US20040029129A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Olsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trwick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.  
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 FILE REFERENCE: ELITRA.04A  
 CURRENT APPLICATION NUMBER: US/10/282,122A  
 CURRENT FILING DATE: 2003-02-20

PRIORITY APPLICATION NUMBER: 601191,078  
 PRIORITY FILING DATE: 2000-03-21  
 PRIORITY APPLICATION NUMBER: 601206,848  
 PRIORITY FILING DATE: 2000-05-23  
 PRIORITY APPLICATION NUMBER: 601207,727  
 PRIORITY FILING DATE: 2000-05-26  
 PRIORITY APPLICATION NUMBER: 601230,335  
 PRIORITY FILING DATE: 2000-09-06  
 PRIORITY APPLICATION NUMBER: 601230,347  
 PRIORITY FILING DATE: 2000-09-09  
 PRIORITY APPLICATION NUMBER: 601242,578  
 PRIORITY FILING DATE: 2000-10-23  
 PRIORITY APPLICATION NUMBER: 601253,625  
 PRIORITY FILING DATE: 2000-11-27  
 PRIORITY APPLICATION NUMBER: 601257,931  
 PRIORITY FILING DATE: 2000-12-22  
 PRIORITY APPLICATION NUMBER: 601267,636  
 PRIORITY FILING DATE: 2001-02-09  
 PRIORITY APPLICATION NUMBER: 601269,308  
 PRIORITY FILING DATE: 2001-02-16  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 78114  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 51529  
 LENGTH: 234  
 TYPE: PRT  
 ORGANISM: Clostridium acetobutylicum  
 US-10-282-122A-51529

RESULT 14  
 US-10-380-430-59  
 Sequence 59, Application US/10380430  
 Publication No. US20040038366A1  
 GENERAL INFORMATION:  
 APPLICANT: UEMORI, Takashi  
 APPLICANT: SATO, Yoshimi  
 APPLICANT: KOBAYASHI, Biji  
 APPLICANT: ASADA, Kiyoko  
 APPLICANT: KATO, Ikuashin  
 TITLE OF INVENTION: THERMOTOLERANT RIBONUCLEASE H  
 FILE REFERENCE: UEMORI=1  
 CURRENT APPLICATION NUMBER: US/10/380,430

Query Match 72.3%; Score 34; DB 15; Length 254;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0;  
Gaps 0;  
Qy 1 GLYPHOMS 9  
|||:  
Db 240 GLYPHOMS 248

Search completed: December 15, 2004, 16:54:13  
Job time : 89.4286 secs

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 GenCore version 5.1.6

Om protein - protein search, using sw model  
 Run on: December 15, 2004, 16:28:26 ; Search time 10.7143 Seconds  
 (without alignments)  
 8.0822 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_113\_121  
 Perfect score: 47  
 Sequence: 1 GLVPIHQMS 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Database : PIR 79; \*  
 1: pir1; \*  
 2: pir2; \*  
 3: pir3; \*  
 4: pir4; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	38	80.9	330	2	I46691	CD86 precursor - rabbit
2	37	78.7	99	2	B8329	C;Species: Oryctolagus cuniculus (domestic rabbit)
3	36	76.6	261	2	A1233	C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
4	35	74.5	434	2	S5579	C;Accession: I46691
5	35	74.5	472	2	A1229	R;Icono, T.; Seto, A.
6	35	74.5	1499	2	AC555	Immunogenetics 42, 217-220, 1995
7	34	72.3	238	2	B7220	A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
8	34	72.3	254	2	B9717	A;Reference number: I46689; MUID:95369849; PMID:7642234
9	34	72.3	263	2	A81446	A;Accession: I46691
10	34	72.3	947	2	B8598	A;Status: preliminary; translated from GB/EMBL/DDBJ
11	34	72.3	1353	2	JC4279	A;Molecule type: mRNA
12	33	70.2	159	2	F8310	A;Residues: 1-330 <ISO>
13	33	70.2	261	2	A51596	A;Cross-references: UNIPROT:P42071; GB:D49842; NID:9755098; PIDN:BA08642.1; PID:975509:
14	33	70.2	278	2	I51324	C;Superfamily: B7-2 antigen
15	33	70.2	405	2	B69200	A;Local Similarity 80.9%; Score 38; DB 2; Length 330; Pred. No. 5.4; Mismatches 0; Indels 0; Gaps 0;
16	33	70.2	407	2	B84609	Best Local Similarity 80.9%; Score 38; DB 2; Length 330; Pred. No. 5.4; Mismatches 0; Indels 0; Gaps 0;
17	33	70.2	411	2	D75408	Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
18	33	70.2	453	2	AH0827	
19	33	70.2	456	2	DR410	
20	33	70.2	718	2	A8352	
21	33	70.2	2018	2	T34274	
22	68.1	105	2	F84609		
23	68.1	109	2	I4096		
24	68.1	134	2	AE3490		
25	68.1	275	2	JC7604		
26	68.1	329	1	A48754		
27	68.1	345	2	T1235		
28	68.1	370	2	FR6236		
29	68.1	391	2	D8926		

#### ALIGNMENTS

Query	Match	Length	DB ID	Description
1 GLVPIHQMS 9	119	GLVPIHQMS 127	146691	RESULT 1 CD86 precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
1 GLVPIHQMS 9	119	GLVPIHQMS 127	146691	RESULT 2 hypothetical protein PA4139 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: B83129 C;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim ,; Lory, S.; Olson, M.V. Nature 406, 939-954, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen A;Reference number: A82950; MUID:20437337; PMID:10954043
1 GLVPIHQMS 9	119	GLVPIHQMS 127	146691	A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-99 <STO> A;Cross-references: UNIPROT:Q9HWP2; GB:AE004830; GB:AE004091; NID:99950337; PIDN:AG075; A;Experimental source: Strain PA01 C;Genetic A;Gene: PA4139
1 GLVPIHQMS 9	1	GLVPIHQMS 9	146691	Query Match 78.7%; Score 37; DB 2; Length 99; Best Local Similarity 66.7%; Pred. No. 2.3; Mismatches 1; Indels 0; Gaps 0; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 57 GLVPIHQLA 65

RESULT 3

AI1233 ribonuclease H rnh homolog rnhB [imported] - *Listeria monocytogenes* (strain SGD-e)

CCSpecies: *Listeria monocytogenes*  
CDate: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
CAccession: AI1233  
R: Glaser, P.; Frangoulis, L.; Buchriser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Encian, K.D.; Fsihi, H.; D.; Jones, L.M.; Kars, U.; Science 294, 849-852, 2001  
A: Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Ma, O.K.; C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
A: Reference number: AB1077; MUID:21537279; PMID:11679669  
A: Accession: AI1233  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-261 <GLA>  
A: Cross-references: UNIPROT:Q8Y7K4; GB:NC\_003210; PIDN: CAC9351.1; PID: g16410689; GSPDB: C: Genetics:  
A: Gene: rnhB  
C: Superfamily: ribonuclease HII  
Query Match 76.6%; Score 36; DB 2; Length 261;  
Best Local Similarity 66.7%; Pred. No. 11; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GLVPIHQLS 9  
DB 238 GLVPIHQLS 246

RESULT 4

S55579 D-nopaline dehydrogenase (EC 1.5.1.19) NoxA - *Agrobacterium tumefaciens*  
CCSpecies: *Agrobacterium tumefaciens*  
CDate: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
CAccession: S55579  
R: Zanker, H.; Lurz, G.; Langridge, U.; Langridge, P.; Schroeder, J.  
Submitted to the EMBL Data Library, February 1994  
A: Description: Octopine and nopaline oxidases from Ti plasmids of *Agrobacterium tumefaciens*  
A: Reference number: S55578  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-434 <ZAN>  
A: Cross-references: UNIPROT:Q59158; EMBL:Z30316; NID: g496533; PIDN: CAA82963.1; PID: g4965  
C: Keywords: oxidoreductase

Query Match 74.5%; Score 35; DB 2; Length 434;  
Best Local Similarity 66.7%; Pred. No. 30; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQLS 9  
DB 262 GLVPIHQLA 270

RESULT 5

A13229 D-nopaline dehydrogenase noxa [imported] - *Agrobacterium tumefaciens* (strain CS8, Dupont)  
CCSpecies: *Agrobacterium tumefaciens*  
CDate: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
CAccession: A13229  
R: Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L.; erage, G.; Gillet, P.; Romer, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Kap, P.; Romer, P.; Zhang, S.; Science 294, 2317-2323, 2001

Query Match 74.5%; Score 35; DB 2; Length 1499;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVPITHQLS 9  
DB 1389 LIPILHQLS 1395

RESULT 7

B72320 ribonuclease HII - *Thermotoga maritima* (strain MSB8)  
CCSpecies: *Thermotoga maritima*  
CDate: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
CAccession: B72320  
A: Status: preliminary  
R: Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haff, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M.  
Nature 399, 323-329, 1999  
A: Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence  
A: Reference number: A72205; MUID: 9287316; PMID: 10360571  
A: Accession: B72320  
A: Status: preliminary  
A: Molecule type: DNA  
A: Residues: 1-238 <KRN>  
A: Cross-references: UNIPROT:Q8X017; GB:AB001755; GB:AE000512; NID: g4981432; PIDN: AAD359  
A: Experimental source: strain MSB8  
C: Genetics:

A:Gene: TM0915  
 C:Superfamily: ribonuclease HII

Query Match 72.3%; Score 34; DB 2; Length 238;  
 Best Local Similarity 55.6%; Pred. No. 24; Mismatches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0; Gaps 0;

Qy 1 GIVPIHQMS 9  
 Db 176 GVULPIIHRUS 184

RESULT 8

E97117 ribonuclease HII [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Accession: E97117 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183: 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum

A;Reference number: A986900; MUID:21359325; PMID:21359325

A;Accession: E97117

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-254 &lt;KUR&gt;

A;Cross-references: UNIPROT:Q97190; GB:AF001437; PIDN:AK79728.1; PID:915024732; GSPDB:G

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CACU762

Query Match 72.3%; Score 34; DB 2; Length 254;

Best Local Similarity 66.7%; Pred. No. 26; Mismatches 6; Conservative 1; Indels 2; Gaps 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLVPIHQMS 9

Db 240 GTTPIHMWS 248

RESULT 9

A81446 acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129) Cjg

C;Species: Campylobacter jejuni \_sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Date: 31-Mar-2000 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C;Accession: A81446 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chillingworth, T.; Quail, M.; Rajandream, M.A.; Rutherford, R.M.; Van Vliet, A.; Whitehead, S.; Barrell, B.; Quail, M.; Rajandream, M.A.; Rutherford, R.M.; Van Vliet, A.; Whitehead, S.; Barrell, B.; Nature: 403: 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp

A;Reference number: A81250; MUID:2135912; PMID:10888204

A;Accession: A81446

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 &lt;PAR&gt;

A;Cross-references: UNIPROT:Q9P1M1; GB:AL139074; GB:AL111168; NIDP:96967505; PIDN:CAB7274

A;Experimental source: serotype O2, strain NCTC 11168

A;Gene: IPXA; Cj0274

C;Superfamily: acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase

C;Keywords: acyltransferase

Query Match 72.3%; Score 34; DB 2; Length 263;

Best Local Similarity 85.7%; Pred. No. 27; Mismatches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPIHQ 7

Db 152 GLTPIHQ 158

H85088 hypothetical protein At4g08830 [imported] - *Arabidopsis thaliana*C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Accession: H85088

R;Anonymous, The European Union *Arabidopsis* Genome Sequencing Consortium, The Cold Spring

Nature 402: 769-771, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: H85088

A;Experimental source: MUID:20083488; PMID:10617198

A;Molecule type: DNA

A;Residues: 1-947 &lt;STD&gt;

A;Cross-references: UNIPROT:Q9LDL8; GB:NC\_001268; NID:97267526; PIDN:CA78008.1; GSPDB:G

A;Genetics: AT4g08830

A;Map position: 4

Query Match 72.3%; Score 34; DB 2; Length 947;

Best Local Similarity 75.0%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LVPHQMS 9

Db 476 LIPHTMS 483

RESULT 11

JC4279

adenylate cyclase (EC 4.6.1.1) type 10 - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C;Accession: JC4279

R;Paterson, J.M.; Smith, S.M.; Harmar, A.J.; Antoni, F.A.

Biochem. Biophys. Res. Commun. 214: 1000-1008, 1995

A;Title: Control of a novel adenylyl cyclase by calcineurin.

A;Reference number: JC4279; MUID:96024597; PMID:7575502

A;Accession: JC4279

A;Molecule type: mRNA

A;Residues: 1-1353 &lt;PAT&gt;

A;Cross-references: UNIPROT:P51810; EMBL:250190

A;Experimental source: AT20 cells

C;Comment: This enzyme is the target of regulation by calcineurin and is a physiologically

messanger molecules.

C;Superfamily: human adenylate cyclase; guanylylate cyclase catalytic domain homology

C;Keywords: phosphorus-oxygen lyase; transmembrane protein

F;118-137:Domain: transmembrane #status predicted &lt;TM01&gt;

F;142-162:Domain: transmembrane #status predicted &lt;TM02&gt;

F;173-193:Domain: transmembrane #status predicted &lt;TM03&gt;

F;230-241:Domain: transmembrane #status predicted &lt;TM04&gt;

F;244-264:Domain: transmembrane #status predicted &lt;TM05&gt;

F;284-304:Domain: transmembrane #status predicted &lt;TM06&gt;

F;311-575:Domain: guanylylate cyclase catalytic domain homology &lt;GCC&gt;

F;787-807:Domain: transmembrane #status predicted &lt;TM07&gt;

F;819-839:Domain: transmembrane #status predicted &lt;TM08&gt;

F;865-885:Domain: transmembrane #status predicted &lt;TM09&gt;

F;891-911:Domain: transmembrane #status predicted &lt;TM10&gt;

F;921-941:Domain: transmembrane #status predicted &lt;TM11&gt;

F;1031-1246:Domain: transmembrane #status predicted &lt;TM12&gt;

F;1037-997:Domain: guanylylate cyclase catalytic domain homology &lt;GCC2&gt;

Query Match 72.3%; Score 34; DB 2; Length 133;

Best Local Similarity 66.7%; Pred. No. 1.7e+02; Mismatches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIVPHQMS 9

Db 1249 GVVPQHQMS 1257

RESULT 10

P83710 hypothetical protein BH0486 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C;Accession: F83710  
 C;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliophilic bacterium *Bacillus halodurans* and  
 A;Reference number: A83650; MUID:2051282; PMID:105832  
 A;Accession: F83710  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-159 <STOP>  
 A;Cross-references: UNIPROT:Q9kFJ3; GB:AP01508; GB:BA000004; NID:g10172890; PIDN:BA042  
 A;Experimental source: strain C-125  
 C;Genetics:  
 C;Gene: BH486  
 C;Superfamily: *Bacillus subtilis* hypothetical protein ytes  
 Query Match 70.2%; Score 33; DB 2; Length 278;  
 Best Local Similarity 71.4%; Pred. No. 46; Mismatches 5; Conservative 2; Gaps 0;  
 Matches 5; Indels 0; Gaps 0;  
 Best Local Similarity 55.6%; Pred. No. 25; Length 159;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GLVPIHQS 9  
 Db 88 GLYPLHEWS 96

RESULT 13  
 AG1596  
 ribonuclease H rnh homolog rnhB [imported] - *Listeria innocua* (strain Clip11262)  
 C;Species: *Listeria innocua*  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AG1595  
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, O.; Domínguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusburgert, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001  
 A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Macueno, E.; Maitournam, A.; Maok, C.; Schliefer, T.; Simoes, N.; Tierre, J.A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Bäcker, O. 179, 7135-7155, 1997  
 A;Title: Comparative genomics of *Listeria* species.  
 A;Reference number: AB1077; MUID:21537279; PMID:11679669  
 A;Accession: AG1596  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-61 <GLA>  
 A;Cross-references: UNIPROT:Q92C79; GB:AL592022; PIDN:CAC96543\_1; PID:g16413785; GSPDB:G  
 A;Experimental source: strain Clip11262  
 C;Genetics:  
 C;Gene: rnhB  
 C;Superfamily: ribonuclease HII  
 Query Match 70.2%; Score 33; DB 2; Length 261;  
 Best Local Similarity 55.6%; Pred. No. 43; Mismatches 5; Conservative 3; Gaps 0;  
 Matches 5; Indels 0; Gaps 0;  
 Qy 1 GLVPIHQS 9  
 Db 238 GLCPIHRLS 246

RESULT 14  
 151324  
 proteolipid protein DM beta - spiny dogfish  
 C;Species: *Squalius acanthias* (spiny dogfish)  
 C;Accession: 151324  
 C;Date: 11-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 R;Kitagawa, K.; Sinoway, M.P.; Yang, C.; Gould, R.M.; Colman, D.R.  
 Neuron 11, 433-448, 1993  
 A;Title: A proteolipid protein gene family: expression in sharks and rays and possible  
 A;Reference number: 151323; MUID:4000010; PMID:83398138  
 A;Accession: 151324  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-278 <KIT>

A;Cross-references: UNIPROT:P316964; EMBL:U02974; NID:9409971; PIDN: AAC59640\_1; PID:g409

C;Superfamily: myelin proteolipid protein

Query Match 70.2%; Score 33; DB 2; Length 278;  
 Best Local Similarity 71.4%; Pred. No. 46; Mismatches 5; Conservative 2; Gaps 0;  
 Matches 5; Indels 0; Gaps 0;

Qy 1 GLVPIHQS 7  
 Db 181 GIVPIHE 187

RESULT 15  
 869200  
 hypothetical protein MTTH749 - *Methanobacterium thermoautotrophicum* (strain Delta H)  
 C;Species: *Methanobacterium thermoautotrophicum*  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: B62200  
 R;Smith, D.R.; Doucette-Samm, L.A.; Dioughey, C.; Lee, H.; Dubois, J.; Aldridge, T.; Qiu, D.; Spadfora, R.; Viccire, R.; Wang, Y.; Wierboski, J.; Mac, J.; Rice, P.; Nelling, J.; Gibson, R.; Jiwani, N.; Spadfora, G.M.; Daniels, C.J.; Mac, J.; Rice, P.; Nelling, J.; Reeve, J.N.; J.; Bäcker, O. 179, 7135-7155, 1997  
 A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: function  
 A;Accession: B62200  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-405 <MTTH>  
 A;Cross-references: UNIPROT:Q26844; GB:AE000853; GB:AE000666; NID:g2621824; PIDN: AAB8525  
 A;Experimental source: strain Delta H  
 C;Genetics:  
 A;Gene: MTTH749  
 Query Match 70.2%; Score 33; DB 2; Length 405;  
 Best Local Similarity 44.4%; Pred. No. 70; Mismatches 4; Conservative 5; Gaps 0;  
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GLVPIHQS 9  
 Db 69 GMMPHQVT 77

Search completed: December 15, 2004, 16:38:00  
 Job time: 13.7143 Secs

OM protein - protein search, using sw model	Run on: December 15, 2004, 16:24:31 ; Search time 49.7143 Seconds (without alignments)				
Perfect score: 47	US-09-868-605-14.COPY_113_121				
Sequence: 1 GLVPIHOMS 9	104.163 Million cell updates/sec				
Scoring table: BLOSUM62					
Searched: Gap0 10.0 , Gapext 0.5					
Total number of hits satisfying chosen parameters: 1825181	1825181				
Minimum DB seq length: 0					
Maximum DB seq length: 200000000					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Listing First 45 summaries					
Database: UniProt 02:*					
1: uniprot_spref:*					
2: uniprot_trembl:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query	Length	DB ID	Description
1	47	100.0	325	2	002838
2	44	93.6	329	2	09SX6
3	44	93.6	332	2	09GM27
4	44	93.6	332	2	095116
5	41	87.2	280	2	09TTF1
6	41	87.2	329	2	09TTF2
7	39	83.0	284	2	09GJ33
8	38	80.9	330	1	0986_RABBIT
9	38	80.9	412	2	099E49
10	37	78.7	99	2	09HWP2
11	37	78.7	378	2	07MD30
12	37	78.7	378	2	09D611
13	37	78.7	812	2	07UFL1
14	36	76.6	90	2	094DX1
15	36	76.6	126	2	099Y03
16	36	76.6	251	2	098IX8
17	36	76.6	261	1	RHE2_L1SMO
18	36	76.6	411	2	06NL37
19	36	76.6	411	2	081QH8
20	36	76.6	411	2	AAS93776
21	36	76.6	1081	2	07UH35
22	36	76.6	6858	2	07QWU1
23	35	74.5	257	1	LRPA_FISHN
24	35	74.5	257	2	07P452
25	35	74.5	314	2	Q7x9M7
26	35	74.5	425	1	YAFP_RHIN
27	35	74.5	434	2	09158
28	35	74.5	472	2	QD2Q8
29	35	74.5	472	2	Q9691
30	35	74.5	472	2	Q8U699
31	34.5	1323	2	Q8SV50	
ALIGNMENTS					
RESULT 1					
ID 002838	PRELIMINARY;	PRT;	325 AA.		
AC 002838;					
DT 01-JUL-1997	(TREMBLrel. 04, Created)				
DT 01-JUL-1997	(TREMBLrel. 04, Last sequence update)				
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)				
DE B7-2.					
GN Name=CD86;					
OS Sus scrofa (Pig).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
OC Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus.					
OC Mammalia; Eutheria;					
OX NCBI_TaxID=9823;					
RN [1]					
SEQUENCE FROM N_A.					
RX MEDLINE:9704772; PubMed:8992613;					
RX Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,					
RA Bothwell A.L.;					
RA "Porcine endothelial CD86 is a major costimulator of xenogeneic human					
RT EMBL; ID=609; AACB1307.1; -.					
DR HSSP; P=2081; INCN.					
RT InterPro; IPR007110; Ig-like.					
RT InterPro; IPR03556; Ig_V.					
DR 09hwp2; P=00047; ig; 1.					
DR SMART; SM00406; IgV; 1.					
DR PROSITE; PS50835; Ig_LIKE; 1.					
SQ SEQUENCE; 325 AA; 35527 MW; 988BEG08137B0597D CRC64;					
Query Match 100.0%; Score 47; DB 2; Length 325;					
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;					
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 GLVPIHOMS 9					
DB 113 GLVPIHOMS 121					
RESULT 2					
ID 09SX6	PRELIMINARY;	PRT;	329 AA.		
AC 09SX6;					
DT 01-NOV-1999	(TREMBLrel. 12, Created)				
DT 01-NOV-1999	(TREMBLrel. 12, Last sequence update)				
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)				
DB CD86 antigen.					
GN Name=CD86;					
OS Felis silvestris catus (Cat).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.					
OC NCAI_TaxID=9685;					
RN [1]					

RP SEQUENCE FROM N\_A.  
 RX MEDLINE=2010222; PubMed=1071336;  
 RA Choi I.-S.; Hash S.M.; Winslow B.J.; Collisson E.W.;  
 RT "Sequence analyses of feline B7 costimulatory molecules.";  
 RL Vet. Immunol. Immunopathol. 73:219-231(2000).  
 RN [2]  
 RP SEQUENCE FROM N\_A.  
 RA Choi I.-S.; Hash S.M.; Winslow B.J.; Collisson E.W.;  
 DR Submitted (JUN 1999) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF15827; AAD2974.1; -.  
 DR KSSP; P42081; INCN.  
 DR InterPro; IPR00110; Ig-like.  
 DR InterPro; IPR00596; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; Ig\_LIKE; 1.  
 DR SEQUENCE 329 AA; 37481 MW; A10521E3C00A0BBB CRC64;  
 Query Match 93.6%; Score 44; DB 2; Length 329;  
 Best Local Similarity 88.9%; Pred. No. 2.2;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 120 GLVPMHQMS 128

RESULT 3  
 Q9GMZ7 PRELIMINARY; PRT; 332 AA.  
 AC 09GMZ7;  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DB 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 GN B-Lymphocyte activation antigen B7-2 (CD86).  
 Name=CD86;  
 OC Felis silvestris catus (Cat).  
 Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 NCBI\_TaxID=9685;  
 RN SEQUENCE FROM N\_A.  
 RP MEDLINE=20102322; PubMed=1102611;  
 RA Nishimura Y., Shimomura M., Miyazawa T., Sato E., Nakamura K.,  
 RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;  
 RT "Molecular cloning of the cDNA encoding the feline B-Lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA-4g,";  
 RL Eur. J. Immunogenet. 27:427-430(2000).  
 DR EMBL; AB03652; BAB1688.1; -.  
 HSSP; P42081; INCN  
 DR InterPro; IPR00110; Ig-like.  
 DR InterPro; IPR00596; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; Ig\_LIKE; 1.  
 DR SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;  
 Query Match 93.6%; Score 44; DB 2; Length 332;  
 Best Local Similarity 88.9%; Pred. No. 2.2;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 120 GLVPMHQMS 128

RESULT 4  
 Q95L16 PRELIMINARY; PRT; 332 AA.  
 ID Q95L16  
 AC 095L16  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CD86.

RP SEQUENCE FROM N\_A.  
 RA Choi I.-S.; Hash S.M.; Winslow B.J.; Collisson E.W.;  
 DR Submitted (JUN 1999) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF15827; AAD2974.1; -.  
 DR KSSP; P42081; INCN.  
 DR InterPro; IPR00110; Ig-like.  
 DR InterPro; IPR00596; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; Ig\_LIKE; 1.  
 DR SEQUENCE 332 AA; 37812 MW; 8BF08B3667D1E3D8 CRC64;  
 Query Match 93.6%; Score 44; DB 2; Length 332;  
 Best Local Similarity 88.9%; Pred. No. 2.2;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 120 GLVPMHQMS 128

RESULT 5  
 Q9TF1 PRELIMINARY; PRT; 280 AA.  
 ID Q9TF1  
 AC Q9TF1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DB 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 GN Truncated B7-2 protein.  
 Name=CD86;  
 OC Canis familiaris (Dog).  
 Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RP SEQUENCE FROM N\_A.  
 RA MEDLINE=2003396; PubMed=1063030;  
 RA Yang S., Sim G.-K.;  
 RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules.";  
 RL Immunogenetics 50:349-353(1999).  
 DR EMBL; AF106827; AAF17298.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR00110; Ig-like.  
 DR InterPro; IPR00306; Ig\_MFC.  
 DR InterPro; IPR03596; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS00835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN 1.  
 DR SEQUENCE 280 AA; 32265 MW; 3C8BBC4D826A7F3 CRC64;  
 SQ

Query Match 87.2%; Score 41; DB 2; Length 280;  
 Best Local Similarity 77.8%; Pred. No. 7.5;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLVPIHQMS 9  
 DB 119 GLVPMHQMS 127

RESULT 6  
 Q9TF2 PRELIMINARY; PRT; 329 AA.  
 ID Q9TF2  
 AC Q9TF2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE B7-2 protein.  
 GN Name=CD86;  
 Canis familiaris (Dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP SPROUCE FROM N.A.  
 RX MEDLINE=20033996; PubMed=10630300;  
 RA Yang S.; Sim G.-K.;  
 RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7  
 molecules.";  
 RL Immunogenetics 50:349-353(1999).  
 DR EMBL; AF106326; RAF1297.1; -.  
 DR HSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR SMART; SW00406; Ig\_V.  
 PROSITE; PS00835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN 1.  
 SEQUENCE 329 AA; 37774 MW; D98BB63437BFT73 CRC64;  
 SQ

Query Match 87.2%; Score 41; DB 2; Length 329;  
 Best Local Similarity 77.8%; Pred. No. 8.8; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPHQMS 9  
 Db 119 GLVPHQMS 127

RESULT 7

QGL33 PRELIMINARY; PRT; 284 AA.  
 ID QGL33  
 AC QGL33;  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE CD86 antigen (Fragment).  
 GN Name=CD86;  
 OS Bos taurus (Bovine).  
 OC Bovaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos; OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RA Brooke G.P.; Howard C.J.; Parsons K.R.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AU291475; CAC1340.1; -.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00477; Ig\_1.  
 DR SMART; SW00406; Ig\_V.  
 PROSITE; PS00290; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell;  
 KW Transmembrane.  
 FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 330 B Lymphocyte activation antigen CD86.  
 FT DOMAIN 23 247 Extracellular (Potential).  
 FT TRANSMEM 248 268 Potential.  
 FT DOMAIN 269 330 Cytoplasmic (Potential).  
 FT DOMAIN 33 127 Ig-like V-type.  
 FT DOMAIN 150 225 Ig-like C2-type.  
 FT DISURID 40 110 Potential.  
 FT DISURID 157 218 Potential.  
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 146 146 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 154 154 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 177 177 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 192 192 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 198 198 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 213 213 N-linked (GlcNAc. . .) (Potential).  
 SQ SEQUENCE 330 AA; 37142 MW; 935CD5C57B3EE1 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 330;  
 Best Local Similarity 77.8%; Pred. No. 3.6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPHQMS 9  
 Db 126 GLVPHQMS 134

RESULT 8

CD86\_RABIT STANDARD; PRT; 330 AA.  
 ID CD86\_RABIT  
 AC P42071;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE B Lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen)  
 DE antigen)  
 GN Name=CD86;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SPROUCE FROM N.A.  
 RX MEDLINE=95369849; PubMed=7542234;  
 RA Isomo T.; Seto A.;  
 RT "Cloning and sequencing of the rabbit gene encoding T-cell  
 costimulatory molecules";  
 RL Immunogenetics 42:217-220(1995).  
 CC !- FUNCTION: Receptor involved in the costimulatory signal essential  
 for T lymphocyte proliferation and interleukin 2 production, by  
 binding CD28 or CT4A. May play a critical role in the early  
 events of T cell activation and costimulation of naive T cells,  
 such as deciding between immunity and anergy that is made by T  
 cells within 24 hours after activation.  
 CC !- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC !- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC !- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; D43842; BAB08642.1; -.  
 DR PIR; I46591.  
 DR HSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR SMART; SW00406; Ig\_V.  
 PROSITE; PS00290; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell;  
 KW Transmembrane.  
 FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 330 B Lymphocyte activation antigen CD86.  
 FT DOMAIN 23 247 Extracellular (Potential).  
 FT TRANSMEM 248 268 Potential.  
 FT DOMAIN 269 330 Cytoplasmic (Potential).  
 FT DOMAIN 33 127 Ig-like V-type.  
 FT DOMAIN 150 225 Ig-like C2-type.  
 FT DISURID 40 110 Potential.  
 FT DISURID 157 218 Potential.  
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 135 135 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 146 146 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 154 154 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 177 177 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 192 192 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 198 198 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 213 213 N-linked (GlcNAc. . .) (Potential).  
 SQ SEQUENCE 330 AA; 37142 MW; 935CD5C57B3EE1 CRC64;

		Best Local Similarity 66.7%; Pred. No. 17; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
RESULT 9		Qy 1 GLVPIHQNS 9	
Q99E49		Db 57 GLVPIHQNL 65	
ID Q99E49; PRELIMINARY; PRT; 412 AA.		Qy 1 GLVPIHQNS 9	
AC Q99E49; Created; 01-JUN-2003 (TREMBLrel. 24, Last sequence update)		Db 57 GLVPIHQNL 65	
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		Qy 1 GLVPIHQNS 9	
DE BLR238		Db 57 GLVPIHQNL 65	
GN OrderedLociNames=blr7238;		Qy 1 GLVPIHQNS 9	
OS Bradyrhizobium japonicum;		Db 57 GLVPIHQNL 65	
OC Bacteria; Proteobacteria; Rhizobiales;		Qy 1 GLVPIHQNS 9	
OC Bradyrhizobiaceae; Bradyrhizobium;		Db 57 GLVPIHQNL 65	
OX NCBI_TaxID=375;		Qy 1 GLVPIHQNS 9	
RN [1] SEQUENCE FROM N.A.		Db 57 GLVPIHQNL 65	
RP STRAIN-USDA110;		Qy 1 GLVPIHQNS 9	
RX MEDLINE=228184998; PubMed=12559275;		Db 57 GLVPIHQNL 65	
RA Kaneko T., Nakamura Y., Saito S., Minamisawa K., Uchiyumi T.,		Qy 1 GLVPIHQNS 9	
RA Sasamoto S., Watanabe A., Idezawa K., Iriuguchi M., Kawashima K.,		Db 57 GLVPIHQNL 65	
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,		Qy 1 GLVPIHQNS 9	
RA Tabata S.; "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.", DNA Res. 9:189-197(2002).		Db 57 GLVPIHQNL 65	
RN DNA Res. 9:189-197(2002).		Qy 1 GLVPIHQNS 9	
DR EMBL; AP002961; BAC52503.1; -.		Db 57 GLVPIHQNL 65	
KW Complete proteome.		Qy 1 GLVPIHQNS 9	
SQ SEQUENCE 412 AA; 43969 MW; B801P68836C8F7BB CRC64;		Db 57 GLVPIHQNL 65	
Query Match 80.9%; Score 38; DB 2; Length 412; Best Local Similarity 66.7%; Pred. No. 45; Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;		Qy 1 GLVPIHQNS 9	
Qy 1 GLVPIHQNS 9		Db 57 GLVPIHQNL 65	
DP 276 GLVPLHKLS 284		Qy 1 GLVPIHQNS 9	
RESULT 10		Db 57 GLVPIHQNL 65	
Q9HWP2		Qy 1 GLVPIHQNS 9	
ID Q9HWP2; PRELIMINARY; PRT; 99 AA.		Db 57 GLVPIHQNL 65	
AC Q9HWP2; Created; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		Qy 1 GLVPIHQNS 9	
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		Db 57 GLVPIHQNL 65	
DT 01-MAR-2003 (TREMBLrel. 24, Last annotation update)		Qy 1 GLVPIHQNS 9	
DE Hypothetical protein.		Db 57 GLVPIHQNL 65	
GN OrderdLociNames=PA1139;		Qy 1 GLVPIHQNS 9	
OS Pseudomonas aeruginosa.		Db 57 GLVPIHQNL 65	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		Qy 1 GLVPIHQNS 9	
OC Pseudomonadaceae; Pseudomonas.		Db 57 GLVPIHQNL 65	
OC NCBI_TaxID=287;		Qy 1 GLVPIHQNS 9	
RN [1] SEQUENCE FROM N.A.		Db 57 GLVPIHQNL 65	
RP STRAIN=ATCC 15992 / PA01; MEDLINE=20437337; PubMed=10984043;		Qy 1 GLVPIHQNS 9	
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Gooley L., Tolentino B., Westbroek-Wadman S., Yuan Y., Brody D.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K., Wu Z., Pulsen I.T., Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.", Nature 406:959-964(2000).		Db 57 GLVPIHQNL 65	
RN Nature 406:959-964(2000).		Qy 1 GLVPIHQNS 9	
DR EMBL; AE004830; AAG07526.1; -.		Db 57 GLVPIHQNL 65	
DR PIR; B83129; B83129; B83129.		Qy 1 GLVPIHQNS 9	
KW Complete proteome; Hypothetical protein.		Db 57 GLVPIHQNL 65	
SQ SEQUENCE 99 AA; 10437 MW; 62706B205463P966 CRC64;		Qy 1 GLVPIHQNS 9	
Query Match 78.7%; Score 37; DB 2; Length 99;		Db 57 GLVPIHQNL 65	
RESULT 11		Qy 1 GLVPIHQNS 9	
Q9MD30		Db 57 GLVPIHQNL 65	
ID Q9MD30; PRELIMINARY; PRT; 378 AA.		Qy 1 GLVPIHQNS 9	
AC Q9MD30; Created; 01-MAR-2004 (TREMBLrel. 26, Last sequence update)		Db 57 GLVPIHQNL 65	
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)		Qy 1 GLVPIHQNS 9	
DE NC-acetylglucosamine-6-phosphate deacetylase.		Db 57 GLVPIHQNL 65	
RN Name=VVA1205;		Qy 1 GLVPIHQNS 9	
OC Vibrio vulnificus (strain YJ016).		Db 57 GLVPIHQNL 65	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;		Qy 1 GLVPIHQNS 9	
OC Vibriaceae; Vibrio.		Db 57 GLVPIHQNL 65	
OX NCBI_TaxID=196600;		Qy 1 GLVPIHQNS 9	
RN [1] SEQUENCE FROM N.A.		Db 57 GLVPIHQNL 65	
RP PubMed=14656955;		Qy 1 GLVPIHQNS 9	
RX Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Su T.-L., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.; "Comparative genome analysis of Vibrio vulnificus, a marine pathogen.", Genome Res. 13:2577-2587(2003).		Db 57 GLVPIHQNL 65	
DR DR; GO:0005448; F:N-acetylglucosamine-6-phosphate deacetylase. . . IEA.		Qy 1 GLVPIHQNS 9	
DR GO; GO:0005448; F:N-acetylglucosamine metabolism; IEA.		Db 57 GLVPIHQNL 65	
DR InterPro; IPR006680; Amidohydro-1.		Qy 1 GLVPIHQNS 9	
DR InterPro; IPR011550; Amidohydro-like.		Db 57 GLVPIHQNL 65	
DR Pfam; PF01979; Amidohydro-1.		Qy 1 GLVPIHQNS 9	
DR Pfam; PD001248; Amidohydro-like. 1.		Db 57 GLVPIHQNL 65	
SQ SEQUENCE 378 AA; 41513 MW; C8E55701F5C2F5BD CRC64;		Qy 1 GLVPIHQNS 9	
Query Match 78.7%; Score 37; DB 2; Length 378; Best Local Similarity 77.8%; Pred. No. 66; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		Db 57 GLVPIHQNL 65	
Qy 1 GLVPIHQNS 9		Db 57 GLVPIHQNL 65	
Db 32 GLVPRHQLS 40		Qy 1 GLVPIHQNS 9	
RESULT 12		Db 57 GLVPIHQNL 65	
Q9D611		Qy 1 GLVPIHQNS 9	
ID Q9D611; PRELIMINARY; PRT; 378 AA.		Db 57 GLVPIHQNL 65	
AC Q9D611; Created; 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		Qy 1 GLVPIHQNS 9	
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		Db 57 GLVPIHQNL 65	
DE N-acetylglucosamine-6-phosphate deacetylase.		Qy 1 GLVPIHQNS 9	
RN OrderdLociNames=VV20736;		Db 57 GLVPIHQNL 65	
OC Vibrio vulnificus.		Qy 1 GLVPIHQNS 9	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;		Db 57 GLVPIHQNL 65	
OC Vibriaceae; Vibrio.		Qy 1 GLVPIHQNS 9	
OX NCBI_TaxID=672;		Db 57 GLVPIHQNL 65	
RN [1] SEQUENCE FROM N.A.		Qy 1 GLVPIHQNS 9	
RP STRAIN=CMCP6;		Db 57 GLVPIHQNL 65	
RC Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choi H.E.; "Complete genome sequence of Vibrio vulnificus CRCP6.;"		Qy 1 GLVPIHQNS 9	
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choi H.E.; "Complete genome sequence of Vibrio vulnificus CRCP6.;"		Db 57 GLVPIHQNL 65	
DR EMBL; AE01831; AAC07668-1; -.		Qy 1 GLVPIHQNS 9	
DR PIR; B83129; B83129; B83129.		Db 57 GLVPIHQNL 65	
KW Complete proteome; Hypothetical protein.		Qy 1 GLVPIHQNS 9	
SQ SEQUENCE 99 AA; 10437 MW; 62706B205463P966 CRC64;		Db 57 GLVPIHQNL 65	
Query Match 78.7%; Score 37; DB 2; Length 99;		Qy 1 GLVPIHQNS 9	

DR GO; GO:0008448; F:N-acetylglucosamine-6-phosphate deacetylase. . ; IEA.  
 DR GO; GO:0006444; P:N-acetylglucosamine metabolism; IEA.  
 DR InterPro; IPR00680; Amidohydro-1.  
 DR InterPro; IPR011550; Amidohydro-Like.  
 DR InterPro; IPR011059; Metalo\_hydrolyase.  
 DR Pfam; PF01979; Amidohydro-1.  
 DR ProDom; PD01248; Amidohydro-like; 1.  
 DR TIGRFAMS; TIGR00221; naga; 1.  
 DR KW Complete proteome. . ; IEA.  
 SQ SEQUENCE 378 AA; 41494 MW; 5084CDA042824B68 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 378;  
 Best Local Similarity 77.8%; Pred. No. 66; Mismatches 7; Conservative 1; Indels 1; Gaps 0; Gaps 0;

Qy 1 GIVIHQMS 9  
 Db 32 GLVPRHQLS 40

RESULT 13

Q7UJF1 PRELIMINARY; PRT; 812 AA.  
 AC Q7UJF1; 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DE Serine/threonine-protein kinase.  
 GN Orderidocustnames=RBL2572;  
 OC Bacteria; Planctomycetacia; Planctomycetales;  
 OC Planctomycetaceae; Pirellulida.  
 OC NCBI\_TaxID=17;  
 [1] SEQUENCE FROM N.A.

RC STRAIN=1; MEDLINE=22735913; PubMed=12835416;  
 RX Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
 RA Schlesner H., Amann R., Reinhardt R.;  
 RT "Complete genome sequence of the marine  
 strain 1." Proc. Natl. Acad. Sci. U.S.A. 100:8288-8303(2003).  
 RL -- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; BX294155; CAD7763.1; -.  
 DR GO; GO:0005524; F1ATP binding; IFA.  
 DR GO; GO:0004674; F1protein Serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F1-transferase activity; IFA.  
 DR GO; GO:0006468; F1protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot kinase.  
 DR InterPro; IPR00821; Ser thr\_pkin\_AS.  
 DR Pfam; PF00069; Pkinase\_1.  
 DR Prosite; PS00001; Prot kinase; 1.  
 DR PROSITE; PS50017; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00018; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Complete proteome; Kinase; Transferase.  
 KW Serine/threonine-protein kinase; Kinase; Transferase.  
 SQ SEQUENCE 812 AA; 90937 MW; C81298D435REAA CRC64;

Query Match 78.7%; Score 37; DB 2; Length 812;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+02; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Gaps 0;

Qy 1 GLVPHQMS 8  
 Db 138 GIVPHQMS 145

RESULT 14

Q84DX1 PRELIMINARY; PRT; 90 AA.

AC Q84DX1; 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Possible VLV repeat protein.  
 OS Tropheryma whipplei (Whipple's bacillus) (Tropheryma whipplei).  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Micrococcineae; Cellulomonadaceae; Tropheryma.  
 OC NCBITaxID=2039;  
 RN [1] SEQUENCE FROM N.A.  
 RX MEDLINE=263243; PubMed=12747404;  
 RA Maiwald M., Lepp P.W., Relman D.A.;  
 RT "Analysis of conserved non-rRNA genes of Tropheryma whipplei.";  
 RL SYST. APPL. MICROBIOL. 26:3-12(2003).  
 DR EMBL; AP83650; AAQ84499.1; -.  
 SQ SEQUENCE 90 AA; 9885 MW; C1D613P55A48B471 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 90;  
 Best Local Similarity 87.5%; Pred. No. 25; Mismatches 7; Conservative 0; Indels 1; Gaps 0; Gaps 0;

Qy 2 LVPHQMS 9  
 Db 25 LVPHQMS 32

RESULT 15

Q89Y03 PRELIMINARY; PRT; 126 AA.  
 AC Q89Y03; 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DE Cytocochrome O ubiquinol oxidase subunit IV.  
 GN Name=cytO; Orderidocustnames=blr0152;  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 OC NCBITaxID=375;  
 RN [1] SEQUENCE FROM N.A.

RC STRAIN=USA110; MEDLINE=2294998; PubMed=12597275;  
 RX Sasaki T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 RA Sasamoto S., Watanabe A., Idesawa K., Iriuchi M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,  
 RA Tabara S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 Bradyrhizobium japonicum USDA110.",  
 RL DNA Res. 9:189-197(2002).  
 DR EMBL; AP005935; BAC154171; COX4\_pro.  
 DR InterPro; IPR005935; BAC154171; COX4\_pro.  
 DR Pfam; PF00626; COX4\_pro; 1.  
 KW Complete proteome. . ; IEA.

SQ SEQUENCE 126 AA; 13951 MW; 919D87A5833BF1BB CRC64;

Query Match 76.6%; Score 36; DB 2; Length 126;  
 Best Local Similarity 75.0%; Pred. No. 35; Mismatches 6; Conservative 2; Indels 0; Gaps 0; Gaps 0;

Qy 2 LVPHQMS 9  
 Db 116 MPHQMS 123

Search completed: December 15, 2004, 16:33:36  
 Job time : 51.7143 secs

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CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for inhibiting costimulation by porcine cells of human T cells, with particular importance in the context of xenotransplantation of porcine organs. Recipients are immunised with hybrid synthetic peptides, such as the present peptide, comprising a T cell epitope conjugated to sequences of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that induce antibodies specific for regions of costimulatory molecules involved in binding to their counter-receptors on human cells are capable of blocking the delivery of costimulation. Once the antibody response has been induced, the transplanted organ will recall this response due to the expression of the costimulatory molecules, thereby sustaining the response, and providing an endogenous mechanism of costimulatory blockade. The method is useful for improving the tolerance of a host to xenografts, particularly porcine pancreatic islet cells. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 29 AA;

Query Match 100.0%; Score 69; DB 3; length 29;

Best Local Similarity 100.0%; Pred. No. 0.00098; Mismatches 0; Indels 0; Gaps 0;

QY 1 C\$TQGYPEPQR 12

Db 18 C\$TQGYPEPQR 29

RESULT 2

AAW14944 AAW14944 standard; protein; 250 AA.

XX

AAW14944;

XX

DT 17-OCT-2003 (revised)

DT 16-JUN-1997 (first entry)

DE

XX

Chimeric human/porcine CD86.

XX

Xenotransplantation; graft rejection; cell interaction; pig; CD68;

KW

monoclonal antibody; chimeric antibody; diagnosis.

XX

Homo; sapiens.

OS

Sus scrofa.

XX

Chimeric.

XX

Key

PT Peptide

PT Protein

PT Region

PT

1..25

/label= Sig\_peptide

26..250

/label= Mat\_protein

246..250

/label= Histidine\_tag

XX

WO9711971-A1.

XX

03-APR-1997.

XX

27-SEP-1996;

96WO-US015575.

XX

PR 28-SEP-1995;

95US 0004489P.

PR 26-SEP-1996;

96US-0004489.

(ALEX-1) ALEXION PHARM INC.

XX

Mueller JP, Evans NJ, Mueller EE, Rollins S, Rother RP, Matis LA;

XX

WPI; 1997-212855/19.

N-PSDB; AAT62939.

XX

Antibodies binding to porcine but not human cell interaction proteins -

useful to treat and assay for rejection of xenografted porcine organs -

tissues or cells.

XX

PS Disclosure; Page 69-70; 105pp; English.

CC A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino acid residues 1-4 and 197-245 from human CD86, and amino acids 5-196 from porcine CD86. It is encoded by a DNA construct (AAT62939) obtained by PCR amplification of porcine sequence and ligation to a sequence encoding the C-terminal region of human CD86 IGC domain. A signal sequence facilitates efficient secretion from transfected mammalian cells.

CC Antibodies to porcine CD86 protein P-selectin (see also AAW14945) and

CC vascular cell adhesion molecule (see also AAW14931-42) are useful for

CC diagnosing human rejection of porcine xenotransplants and for improving

CC xenotransplantation of porcine cells, tissues and organs into human

CC recipients. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 250 AA;

Query Match 100.0%; Score 69; DB 2; length 250;

Best Local Similarity 100.0%; Pred. No. 0.0081; Mismatches 0; Indels 0; Gaps 0;

QY 1 C\$TQGYPEPQR 12

Db 157 C\$TQGYPEPQR 168

RESULT 3

AAV95321 AAV95321 standard; protein; 325 AA.

XX

AAV95321;

XX

DT 25-SEP-2000 (first entry)

XX

DE Pig costimulatory molecule CD86 (B7-2).

XX

KW Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;

XX

xenotransplantation; organ transplant; vaccine; epitope.

XX

OS Sub scrofa.

XX

FH Key location/Qualifiers

FT Peptide 17..29 /note= "Peptide 9"

FT Peptide 21..32 /note= "Peptide 8"

FT Peptide 32..40 /note= "Peptide 2"

FT Peptide 76..88 /note= "Peptide 10"

FT Peptide 81..90 /note= "Peptide 1"

FT Peptide 94..104 /note= "Peptide 5"

FT Peptide 109..121 /note= "Peptide 3"

FT Peptide 113..121 /note= "Peptide 4"

FT Peptide 151..162 /note= "Peptide 6"

XX

W020037102-A2.

XX

29-JUN-2000.

XX

PR 17-DEC-1999; 99WO-GB004200.

XX

19-DEC-1998; 99GB-00027921.

XX

23-OCT-1999; 99GB-00025015.

XX

(MLM-) ML LAB PLC.

XX

Lechler RI, Rogers NJ, Dorling A;

XX

DR WPI; 2000-442537/38.  
DR N-PSDB; AIA9661.

XX Novel methods for improving tolerance to a xenograft comprising

PT immunizing a mammal with a T-cell epitope and a B-cell epitope.

XX Disclosure; Fig 6; 81pp; English.

XX The present sequence is that of pig co-stimulatory molecule CD85 (B7-2),  
CC as deduced from an isolated cDNA clone (see AAY9661). CD85 plays a key  
role in T cell costimulation. The invention relates to a novel strategy  
for inhibiting costimulation by porcine cells of human T cells, with  
particular importance in the context of xerortransplantation of porcine  
CC organs. Recipients are immunised with hybrid synthetic peptides  
comprising a T cell epitope conjugated to sequences of the porcine  
CC costimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86  
(see also AAY952533). Peptides that induce antibodies specific for regions of  
CC costimulatory molecules involved in binding to their counter-receptors on  
CC receptors on human cells (CD28 and CD14) are capable of blocking the delivery of  
CC delivery of costimulation. Once the antibody response has been induced, the  
CC transplanted organ will recall this response due to the expression of the  
CC costimulatory molecules, thereby sustaining the response, and providing  
CC providing an endogenous mechanism of costimulatory blockade. The method  
is useful for improving the tolerance of a host to xenografts,  
CC particularly porcine pancreatic islet cells

XX Sequence 325 AA;

Query Match 100.0%; Score 69; DB 3; Length 325;  
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 C5STQGYPPQR 12  
Db 151 C5STQGYPPQR 162

RESULT 4

AY95324 AAY95324 standard; protein; 325 AA.

AC AAY95324;

XX 25-SEP-2000 (first entry)

DB Human costimulatory molecule CD86 (B7-2).

XX Co-stimulatory molecule; CD86; B7-2; human; immunosuppressive;  
KW xerotransplantation; organ transplant; vaccine; epitope.

OS Homo sapiens.

XX Key location/Qualifiers  
FH Peptide 19..42  
FT /note= "epitope"

FT Peptide 53..73  
FT /note= "epitope"  
FT Peptide 101..129  
FT /note= "epitope"  
FT Peptide 136..165  
FT /note= "epitope"

XX WO20031102A2.  
XX 29-JUN-2000.  
XX 17-DEC-1999; 99W0-GB004200.  
XX 19-DBC-1998; 98GB-00027921.  
XX 23-OCT-1999; 99GB-00025015.  
XX (MLML-) ML LAB PLC.

PI Lechner RI, Rogers NJ, Dorling A;  
XX WPI; 2000-442537/38.

XX Novel methods for improving tolerance to a xenograft comprising

PT immunizing a mammal with a T-cell epitope and a B-cell epitope.

XX Disclosure; Fig 26; 81pp; English.

XX The present sequence is that of human co-stimulatory molecule CD86 (B7-  
CC 2). CD86 plays a key role in T cell costimulation. The invention relates  
to a novel strategy for inhibiting costimulation by porcine cells of  
CC human T cells, with particular importance in the context of  
CC xerotransplantation of porcine organs. Recipients are immunised with  
CC hybrid synthetic peptides comprising a T cell epitope conjugated to  
CC sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see  
CC AAY95321-24). Peptides that induce antibodies specific for regions of  
CC costimulatory molecules involved in binding to their counter-receptors on  
CC human cells (CD28 and CD14) are capable of blocking the delivery of  
CC costimulation. Once the antibody response has been induced, the  
CC transplanted organ will recall this response due to the expression of the  
CC costimulatory molecules, thereby sustaining the response, and providing  
CC an endogenous mechanism of costimulatory blockade. The method is useful  
CC for improving the tolerance of a host to xenografts, particularly porcine  
CC pancreatic islet cells

XX Sequence 325 AA;

Query Match 100.0%; Score 69; DB 3; Length 325;  
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 C5STQGYPPQR 12  
Db 151 C5STQGYPPQR 162

RESULT 5

AY41078 AAY41078 standard; protein; 280 AA.

AC AAY41078;

XX 20-DEC-1999 (first entry)

DB Canine B7-2S protein.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;  
KW allergic reaction; infectious disease; tumor development; canine;  
KW graft refection; inflammation; arthritis; atopic dermatitis;  
XX OS Canis familiaris.

XX Key location/Qualifiers  
FH Peptide 19..42  
FT /note= "epitope"

FT Peptide 53..73  
FT /note= "epitope"  
FT Peptide 101..129  
FT /note= "epitope"  
FT Peptide 136..165  
FT /note= "epitope"

XX WO9947558A2.  
XX 23-SEP-1999.  
XX 19-MAR-1999; 99W0-US06187.  
XX 19-MAR-1999; 98US-0078765P.  
XX 17-APR-1998; 98US-0062597.  
XX PA (HESKA) HESKA CORP.  
XX Sim G, Yang S, Sellins KS;  
XX WPI; 1999-571822/4B.  
XX DR N-PSDB; AIA227923.  
XX DR New isolated B7 and CTLA4 nucleic acids, used to develop products for  
PT treating, e.g. autoimmune and atopic diseases.  
XX PA Claim 4; Page 109-111; 148pp; English.

XX  
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such as humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening  
 XX  
 Sequence 280 AA;

Query Match 78.3%; Score 54; DB 2; Length 280;  
 Best Local Similarity 81.8%; Pred. No. 2.2; Mismatches 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CSSTQ3GPFEPQ 11  
 DB 158 CSSIQGYPEPK 168

RESULT 6  
 AAY41076 AAY41076 standard; protein, 329 AA.  
 XX  
 AC AAY41076;  
 XX  
 DT 20-DEC-1999 (first entry)  
 DE Cat CD86 (B7-2) ligand.  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 15-FEB-2000 (first entry)  
 DE Cat CD86 (B7-2) ligand.  
 XX  
 KW CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;  
 KW feline leukaemia virus; feline infectious peritonitis virus;  
 KW feline panleukopenia virus; feline calicivirus; feline reovirus-3;  
 KW feline sarcoma virus; feline herpesvirus; feline Born disease;  
 KW rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;  
 KW parasite; autoimmune disease; transplant rejection; therapy.  
 XX  
 OS Felis catus.  
 XX  
 PN W09957271-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PR 30-APR-1999; 99WO-US009502.  
 XX  
 PR 01-MAY-1998; 98US-00071699.  
 XX  
 PA (TEXA ) TEXAS A & M SYSTEM.  
 XX  
 PI Collison EW, Hash SM, Choi I;  
 XX  
 DR WPI; 2000-052972/04.  
 XX  
 N-PSDB; AA234785.

PS Example 1A; FIG 3A; 186PP; English.

XX  
 CC The present sequence represents feline CD86 (B7-2) ligand, as predicted  
 CC from isolated cDNA of peripheral blood mononuclear cells. The  
 CC coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279)  
 CC and a tumour antigen or an antigen from a pathogenic organism has the  
 CC ability to activate or enhance activation of T-lymphocytes. Coexpression  
 CC of CD86 with CTLA-4 (see AAY2280) has the ability to regulate activation  
 CC of T-lymphocytes. The invention provides isolated nucleic acids encoding  
 CC feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or  
 CC feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic  
 CC acids and polypeptides encoded by the nucleic acids. It also provides  
 CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and  
 CC further comprising immunogens derived from pathogens, especially feline  
 CC immunodeficiency virus (FIV), feline leukaemia virus, feline infectious  
 CC peritonitis virus, feline panleukopenia virus, feline calicivirus,  
 CC feline reovirus-3, feline rotavirus, feline coronavirus, feline coronavirous, feline  
 CC virus, feline sarcoma virus, feline herpesvirus, feline Born disease  
 CC viruses, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria  
 CC immitis, or a flea, bacterial pathogen, or parasite (all claimed).  
 CC Vaccines capable of enhancing an immune response, and vaccines capable of  
 CC suppressing an immune response (suitable for treating an autoimmune  
 CC disease or tissue or organ transplant rejection) are claimed. (Updated on  
 CC 12-SEP-2003 to standardise OS field)

SQ Sequence 329 AA;

Query Match 78.3%; Score 54; DB 2; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 2.6; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CSSTQ3GPFEPQ 11  
 DB 158 CSSIQGYPEPK 168

RESULT 7  
 AAY32278 standard; protein, 329 AA.  
 XX  
 ID AAY32278  
 AC AAY32278;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 15-FEB-2000 (first entry)  
 DE Cat CD86 (B7-2) ligand.  
 XX  
 KW CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;  
 KW feline leukaemia virus; feline infectious peritonitis virus;  
 KW feline panleukopenia virus; feline calicivirus; feline reovirus-3;  
 KW feline sarcoma virus; feline herpesvirus; feline Born disease;  
 KW rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;  
 KW parasite; autoimmune disease; transplant rejection; therapy.  
 XX  
 OS Felis catus.  
 XX  
 PN W09957271-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PR 30-APR-1999; 99WO-US009502.  
 XX  
 PR 01-MAY-1998; 98US-00071699.  
 XX  
 PA (TEXA ) TEXAS A & M SYSTEM.  
 XX  
 PI Collison EW, Hash SM, Choi I;  
 XX  
 DR WPI; 2000-052972/04.  
 XX  
 N-PSDB; AA234785.

PS Example 1A; FIG 3A; 186PP; English.

XX  
 CC The present sequence represents feline CD86 (B7-2) ligand, as predicted  
 CC from isolated cDNA of peripheral blood mononuclear cells. The  
 CC coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279)  
 CC and a tumour antigen or an antigen from a pathogenic organism has the  
 CC ability to activate or enhance activation of T-lymphocytes. Coexpression  
 CC of CD86 with CTLA-4 (see AAY2280) has the ability to regulate activation  
 CC of T-lymphocytes. The invention provides isolated nucleic acids encoding  
 CC feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or  
 CC feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic  
 CC acids and polypeptides encoded by the nucleic acids. It also provides  
 CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and  
 CC further comprising immunogens derived from pathogens, especially feline  
 CC immunodeficiency virus (FIV), feline leukaemia virus, feline infectious  
 CC peritonitis virus, feline panleukopenia virus, feline calicivirus,  
 CC feline reovirus-3, feline rotavirus, feline coronavirus, feline coronavirous, feline  
 CC virus, feline sarcoma virus, feline herpesvirus, feline Born disease  
 CC viruses, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria  
 CC immitis, or a flea, bacterial pathogen, or parasite (all claimed).  
 CC Vaccines capable of enhancing an immune response, and vaccines capable of  
 CC suppressing an immune response (suitable for treating an autoimmune  
 CC disease or tissue or organ transplant rejection) are claimed. (Updated on  
 CC 12-SEP-2003 to standardise OS field)

SQ Sequence 329 AA;



DE Feline CD86 protein.

XX KW Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;

XX feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;

XX CTLA-4; vaccine; rabies; autoimmune disease; organ transplant;

XX toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukaemia;

XX feline calicivirus; rotavirus; reovirus type 3; coronavirus; herpes;

XX bovine disease.

OS Felis sp.

XX Felis catus.

XX US2002028208-A1.

XX PN 07-MAR-2002.

XX XX 30-APR-1999; 99US-00303510.

XX XX 01-MAY-1998; 98US-0083869P.

XX XX (COLL1) COLLISSON E W.

PA (HASH1) HASH S M.

PA (CHO1) CHOI I.

PA (HASH1) HASH S M.

PA (CHO1) CHOI I.

PA (HASH1) HASH S M.

PA (CHO1) CHOI I.

PA (HASH1) HASH S M.

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PA (CHO1) CHOI I.

PA (HASH1) HASH S M.

PA (CHO1) CHOI I.

PA (HASH1) HASH S M.

AC AAV41079;

XX DT 20-DEC-1999 (first entry)

XX DE Feline B7-2 protein.

XX KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; feline graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX OG Felis catus.

XX PN WO9947558-A2.

XX PD 23-SEP-1999.

XX PR 19-MAR-1999; 99WO-US006187.

XX PR 19-MAR-1998; 98US-0078765P.

XX PR 17-APR-1998; 98US-0006599T.

XX DR WPI; 1999-571822/48.

XX PA (HESK1) HESKA CORP.

XX PI Sim G, Yang S, Sellins KS;

XX DR WPI; 1999-571822/48.

XX PT New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases.

XX PS Claim 4; Page 116-119; 148pp; English.

XX SQ The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such as humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.

XX Sequence 332 AA;

Query Match 78.3%; Score 54; DB 2; length 332;

Best Local Similarity 81.8%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 csgtqgyppqo 11

D<sub>b</sub> 159 csgtqgyppk 169

RESULT 12

AAW08473 standard; protein; 102 AA,

XX AAW08473;

AC AAW08473;

XX DT 08-APR-1997 (first entry)

XX DE Human B lymphocyte antigen B7-2 constant region.

XX DB Human B lymphocyte antigen B7-2 constant region.

XX KW CTLA4; CD28; ligand; B7-2; B lymphocyte antigen; B-cell; costimulation; immunoglobulin; antibody; autoimmune disease; allergy; tumour; vaccine; graft versus host disease; T-cell; T lymphocyte; TH2 response; immunosuppressive; immunostimulant; therapy.

XX OS Homo sapiens.

XX PN WO9640915-A2.

PD 19-DEC-1996.  
 XX  
 PP 06-JUN-1996; 96WO-US009052.  
 XX  
 PR 07-JUN-1995; 95US-00479744.  
 XX  
 PR (DAND ) DANA FARBER CANCER INST INC.  
 PA (REPK ) REPLICEN CORP.  
 XX  
 PI Freeman GJ, Nadler LM, Gray GS;  
 XX  
 PR WI; 1997-077269/07.  
 DR N-FSDB; AT49198.  
 XX  
 PT DNA encoding a B7-2 fusion protein - used to enhance or down regulate B lymphocyte antigens.  
 XX  
 PS Example 7D; Page 124; 171pp; English.  
 XX  
 CC A cDNA clone (AT49198) codes for the constant region-like domain (AAW8467) of human B-lymphocyte antigen B7-2 (see also AAW8467), a CTLA4/CD28 ligand which costimulates T cell activation. It was obtid. by PCR amplification (see also AT49604-05) and cloned into pRSB5HIG1. B7-2 constant region-IGG1 constant region fusion protein, B7-2IGG1, was expressed in COS and CHO cells. Such fusion proteins can be used to suppress T cell-mediated immune responses.  
 CC  
 CC Sequence 102 AA;  
 CC  
 CC Query Match 73.9%; Score 51; DB 2; Length 102;  
 CC Best Local Similarity 66.7%; Pred. No. 2.4;  
 CC Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 CC Qy 1 CSSRQGYRPPQR 12  
 CC 24 CSSIHYGYPEPKK 35  
 CC SQ Sequence 102 AA;  
 CC  
 RESULT 13  
 DE AAB37093  
 ID AAB37093 standard; protein; 102 AA.  
 XX  
 AC AAB37093;  
 XX  
 DT 28-MAR-2001 (first entry)  
 DE Human B7-2 constant domain.  
 XX  
 KW Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28; antigen; extracellular domain; CTLA4; immunoglobulin constant region; immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage; T cell-mediated immune response; transplantation; vaccination; fusion construct.  
 KW  
 OS Homo sapiens.  
 XX  
 US6130316-A.  
 PD 10-OCT-2000.  
 XX  
 PR 26-JUL-1994; 94US-00280757.  
 XX  
 PR 26-JUL-1993; 93US-00109393.  
 PR 19-AUG-1993; 93US-00109393.  
 PR 03-NOV-1993; 93US-00147773.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (REPK ) REPLICEN CORP.  
 XX  
 PI Freeman GJ, Nadler LM, Gray GS, Greenfield B;  
 DR WPI; 2000-655681/63.  
 DR N-PSDB; AAC84083.

---

XX  
 PT Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for enhancing or suppressing T cell-mediated immune response, especially during tissue, skin or organ transplantation, or in graft-versus-host disease.  
 XX  
 PS Example 7; Col 105-106; 83pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule encoding a fusion protein comprising a first nucleotide sequence encoding a first peptide, and a second nucleotide sequence encoding a second peptide. The first nucleotide sequence hybridizes in 6 X sodium chlorides/sodium citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C to a portion of a nucleotide sequence which encodes a human or murine B lymphocyte antigen (B7-2) extracellular domain. The first peptide has the ability to bind CD28 or CTLA4. The first peptide has an amino acid sequence that is identical or at least 50% identical with the extracellular domain of a human B7-2 peptide (HAB7085). This sequence represents the human B7-2 constant domain, used for generating an B7-2/IG fusion construct. The nucleic acid molecules are useful in various expression vectors to direct synthesis of the corresponding proteins or peptides in a variety of hosts, particularly eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic acids are also useful for enhancing the immunogenicity of a mammalian cell, e.g. tumour cell (sarcoma) or an antigen presenting cell (macrophage). The fusion proteins or peptides are useful for enhancing or suppressing T cell-mediated immune responses, e.g. in situations of tissue, skin or organ transplantation, or in graft-versus-host disease. The proteins are also useful for enhancing the efficacy of vaccination against a variety of pathogens, and may also be used to upregulate an immune response against a particular pathogen during an infection or against a tumour in a tumour -bearing host.  
 XX  
 CC Sequence 102 AA;  
 CC  
 CC Query Match 73.9%; Score 51; DB 3; Length 102;  
 CC Best Local Similarity 66.7%; Pred. No. 2.4;  
 CC Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 CC Qy 1 CSSRQGYRPPQR 12  
 CC 24 CSSIHYGYPEPKK 35  
 CC SQ Sequence 102 AA;  
 CC  
 RESULT 14  
 DE AAW30209  
 ID AAW30209 standard; protein; 244 AA.  
 XX  
 AC AAW30209;  
 XX  
 DT 10-MAY-1999 (first entry)  
 DE hB7.1hs soluble fusion protein.  
 XX  
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; autoimmune disease; allergy; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; hB7.1hs.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key <sup>15</sup>  
 FH Peptide 1..23  
 FT <sup>1</sup>  
 FT <sup>2</sup>  
 FT <sup>24..238</sup>  
 FT Domain  
 FT <sup>1</sup>  
 FT <sup>2</sup>  
 FT Peptide  
 FT <sup>239..244</sup>  
 FT <sup>1</sup>  
 XX <sup>1</sup>  
 WO95B965-A2.

XX	30-DEC-1998.
2D	22-JUN-1998; 98WO-EP003791.
XX	20-JUN-1997; 97EP-0087092.
PR	(INNO-) INNOGENETICS NV.
XX	Lorre K, Sablon E, Buyse M, Bosman A;
PR	WPI; 1999-105615/09.
PT	New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection.
PS	Example 3.1.3; Fig 5; 182pp; English.
XX	This 28 kDa soluble fusion protein, termed hB7.2his, is composed of human hexahistidine detection/purification tag. It was produced by PCR amplification (see AXL0103-04) of hB7.2 cDNA in pcDNAhB7.2 (ICGG2307), insertion of the PCR fragment into baculovirus vector PACSG2 and expression in <i>Spodoptera frugiperda</i> insect cells. The invention relates to molecules such as diabodies, trivalent and tetravalent antibodies and small antigen binding peptides which can cross-link, or cross-react with, B7.1 and B7.2 expressed on professional antigen presenting cells leading to the inhibition of antigen-specific T cell activation. Methods to produce such molecules are provided. The molecules are used to treat or prevent diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).
XX	Sequence 244 AA;
Query Match	73.9%; Score 51; DB 2; length 244;
Best Local Similarity	55.7%; Pred: No. 5.7;
Matches	8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy	1 CSSTQYPEPQR 12
Db	151 CSSTQYPEPQRK 162
RESULT 15	
DT	AAW86005 standard; protein; 246 AA.
XX	
AC	AAW86005;
XX	
15-MAR-1999	(first entry)
DT	Human B7-2 extracellular domain and linker.
XX	
KW	Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; mouse; human; B7-2; co-stimulatory molecule.
KW	Homo sapiens.
OS	Synthetic.
OS	Chimeric.
XX	
PH	Location/Qualifiers
FT	1. 16 .
FT	/label= Sig_peptide
FT	Protein
FT	17. 241 .
FT	/label= Mat_protein
FT	/note= "B7-2 extracellular domain"
FT	Peptide
FT	242. 245 .
XX	/label= Linker
PN	W09855607-A2.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: December 15, 2004, 16:29:06 ; (without alignments) ; Search time 20.5714 Seconds ; 38.685 Million cell updates/sec

Title: US-09-868-605-14\_COPY\_151\_162

Perfect score: 69

Sequence: 1 CSSTQGYPERQ 12

Scoring table: BLOSUM62

GapPenalty: 10.0 , GapExt: 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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2: /cgn2\_6/prodata/1/iaa/5B\_COMB\_pep:\*

3: /cgn2\_6/prodata/1/iaa/6A\_COMB\_pep:\*

4: /cgn2\_6/prodata/1/iaa/6B\_COMB\_pep:\*

5: /cgn2\_6/prodata/1/iaa/PC105\_COMB\_pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
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2	54	78.3	329	4	US-09-651-200-18
3	54	78.3	329	4	US-09-651-200-19
4	54	78.3	329	4	US-09-651-010-06
5	51	73.9	102	3	US-08-479-714A-47
6	51	73.9	102	3	US-08-280-717B-47
7	51	73.9	102	4	US-09-425-205-47
8	51	73.9	323	4	US-09-651-200-21
9	51	73.9	323	4	US-09-441-411-22
10	51	73.9	323	5	PTC-US94-09442-2
11	51	73.9	324	4	US-09-910-174B-6
12	51	73.9	324	4	US-09-20-451-6
13	51	73.9	329	2	US-08-456-104-2
14	51	73.9	329	2	US-08-101-624-2
15	51	73.9	329	3	US-08-479A-4
16	51	73.9	329	3	US-08-280-717B-2
17	51	73.9	329	3	US-08-05-657A-23
18	51	73.9	329	3	US-08-472-555-23
19	51	73.9	329	3	US-08-403-233A-4
20	51	73.9	329	4	US-09-657-115-32
21	51	73.9	329	4	US-09-425-16A-4
22	51	73.9	329	4	US-09-425-765-2
23	51	73.9	329	4	US-09-837-867A-23
24	51	73.9	4	US-09-205-112-2	
25	51	73.9	329	4	US-09-411-411-26
26	51	73.9	329	4	PCT-US95-02576-23
27	51	73.9	351	4	US-09-756-993-18

ALIGNMENTS

RESULT 1

US-09-651-200-20

; Sequence 20, Appl ; Sequence 20, Application US/09651200 ; Patent No. 6429303

; GENERAL INFORMATION:

; APPLICANT: Green et al.

; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B

; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and

; TITLE OF INVENTION: Polypeptides Encoded Thereby

; FILE REFERENCE: 15966-562 (CURA-62)

; CURRENT APPLICATION NUMBER: US/09/651,200

; CURRENT FILING DATE: 2000-03-30

; PRIOR APPLICATION NUMBER: 60/152383

; PRIOR FILING DATE: 1999-09-03

; PRIOR APPLICATION NUMBER: 60/172909

; PRIOR FILING DATE: 1999-12-21

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 325

; TYPE: PRT

; ORGANISM: sus sp.

; US-09-651-200-20

Query Match 100.0% ; Score 69 ; DB 4 ; Length 325 ; Best Local Similarity 100.0% ; Pred. No. 0.0013 ; Matches 12 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Caps 0 ; Seq 1 CSSTQGYPERQ 12

Db 151 CSSTQGYPERQ 162



RESULT 6  
 US-09-280-757B-47  
 Sequence 47, Application US/08280757B  
 Patent No. 6130316  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 APPLICANT: Greenfield, Edward  
 TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and  
 TITLE OF INVENTION: Uses Therefor  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/280,757B  
 APPLICATION NUMBER: US/08/280,757B  
 FILING DATE: 26-JUL-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/101,624  
 FILING DATE: 26-JULY-1993  
 APPLICATION NUMBER: 08/109,393  
 FILING DATE: 19-AUG-1993  
 APPLICATION NUMBER: 08/147,773  
 FILING DATE: 3-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REFERENCE/DOCKET NUMBER: RPI-004CP2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-7400  
 INFORMATION FOR SEQ ID NO: 47:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 102 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-425-762-47  
 Query Match 73.9%; Score 51; DB 3; Length 102;  
 Best Local Similarity 66.7%; Pred. No. 0.34; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CSSTQGYPERQR 12  
 Db 24 CSSTQGYPERK 35  
 US-09-425-762-47  
 RESULT 7  
 US-09-651-200-21  
 Sequence 21, Application US/09651200  
 Patent No. 6429303  
 GENERAL INFORMATION:  
 APPLICANT: Green et al  
 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 TITLE OF INVENTION: Polypeptides Encoded Thereby  
 FILE REFERENCE: 15866-562 (CTRA-62)  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 CURRENT FILING DATE: 2000-08-30  
 PRIOR APPLICATION NUMBER: 6/0152383  
 PRIOR FILING DATE: 1999-09-03  
 PRIOR APPLICATION NUMBER: 6/0172909  
 PRIOR FILING DATE: 1999-12-21  
 PRIOR APPLICATION NUMBER: 6/0183578  
 PRIOR FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 21  
 LENGTH: 323  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-651-200-21  
 Query Match 73.9%; Score 51; DB 4; Length 323;  
 Best Local Similarity 66.7%; Pred. No. 1.1; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CSSTQGYPERQR 12  
 Db 24 CSSTQGYPERK 35  
 RESULT 7  
 US-09-425-762-47  
 Sequence 47, Application US/09425762  
 Patent No. 6605579  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: No. 6605579el CTLA4/CD28 Ligands and  
 TITLE OF INVENTION: Uses Therefor  
 NUMBER OF SEQUENCES: 55  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP

Db 151 CSSIHGYPEPK 162

RESULT 9  
US-09-441-411-22  
Sequence 22, Application US/09441411  
Patent No. 6731172  
GENERAL INFORMATION:  
APPLICANT: Scholler, Nathalie B.  
APPLICANT: Disis, Mary L.  
APPLICANT: Hellström, Ingegerd  
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
FILE REFERENCE: 730033.409  
CURRENT APPLICATION: US/09/441.411  
CURRENT FILING DATE: 1999-11-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-441-411-22

Query Match 73.9%; Score 51; DB 4; Length 323;  
Best Local Similarity 66.7%; Pred. No. 1.1; 2; Mismatches 2; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Missmatches 2; Indices 0; Gaps 0;

Qy 1 CSSTQGYPEPOR 12  
Db 151 CSSIHGYPEPK 162

RESULT 10  
PCT-094-09642-2  
Sequence 2, Application PC/US9409642

GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding  
NUMBER OF SEQUENCES: 2  
TITLE OF INVENTION: Protein and Related Reagents  
CORRESPONDENCE ADDRESS:  
ADRESSEER: Schering-Plough Corporation, M-3-W  
STREET: One Giralta Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940-1000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: Apple Macintosh IICi  
OPERATING SYSTEM: System Software 7.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09642  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/120,606  
FILING DATE: 13-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,882  
FILING DATE: 03-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Blasdale, John H. C.  
REGISTRATION NUMBER: 31,895  
REFERENCE/DOCKET NUMBER: DX0390K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-822-7398  
TELEFAX: 201-822-7039  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids

RESULT 11  
US-09-910-174B-6  
Sequence 6, Application US/09910174B  
Patent No. 6630575  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
FILE REFERENCE: 5800/236924  
CURRENT APPLICATION NUMBER: US/09/910,174B  
CURRENT FILING DATE: 2001-07-20  
PRIORITY APPLICATION NUMBER: US 09/620,461  
PRIORITY FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-910-174B-6

Query Match 73.9%; Score 51; DB 4; Length 324;  
Best Local Similarity 66.7%; Pred. No. 1.1; 2; Mismatches 2; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Missmatches 2; Indices 0; Gaps 0;

Qy 1 CSSTQGYPEPOR 12  
Db 151 CSSIHGYPEPK 162

RESULT 12  
US-09-620-461-6  
Sequence 6, Application US/09620461  
Patent No. 6635750  
GENERAL INFORMATION:  
APPLICANT: Coyle, Anthony J.  
APPLICANT: Fraser, Christopher C.  
APPLICANT: Manning, Stephen  
TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
FILE REFERENCE: 5800-149  
CURRENT APPLICATION NUMBER: US/09/620,461  
CURRENT FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-620-461-6

Query Match 73.9%; Score 51; DB 4; Length 324;  
Best Local Similarity 66.7%; Pred. No. 1.1; 2; Mismatches 2; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Missmatches 2; Indices 0; Gaps 0;

Qy 1 CSSTQGYPEPOR 12  
Db 151 CSSIHGYPEPK 162

Db 151 CSSIHGYPEPKK 162

RESULT 13

US-08-456-104-2

; Sequence 2, Application US/08456104

; Patent No. 5,851310

; GENERAL INFORMATION:

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LARIVE &amp; COCKFIELD

; CITY: 60 State Street, Suite 510

; STATE: Massachusetts

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/101,624

; FILING DATE: 26-JUL-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/101,624;

; FILING DATE: 26-JUL-1993;

; APPLICATION NUMBER: 08/109,393;

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: 36,207

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 329 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-101-624-2

; Sequence 2, Application US/08456104

; Patent No. 6084067

; GENERAL INFORMATION:

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; TITLE OF INVENTION: Gray, Gary S.

; TITLE OF INVENTION: Uses Therefor

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LARIVE &amp; COCKFIELD

; CITY: 60 State Street, Suite 510

; STATE: Massachusetts

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/479,744A

; FILING DATE: June 7, 1995

; CLASSIFICATION: 515

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/280,757

; FILING DATE: 26-JUL-1994

; APPLICATION NUMBER: 08/109,393

; FILING DATE: 28-AUG-1993

; APPLICATION NUMBER: 08/101,624

; FILING DATE: 26-JULY-1993

APPLICATION NUMBER: 08/147,773  
FILING DATE: 3-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: RPI-004CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-9411  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-479-744A-2

Query Match 73.9%; Score 51; DB 3; Length 329;  
Best Local Similarity 66.7%; Pred. No. 1.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
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||| |||||: 157 OSSINGYPEPK 168  
Db

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Job time : 20.5714 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 15, 2004, 16:37:44 (Search time 116.571 Seconds (Without alignments))

US-09-868-605-14\_COPY\_151\_162

US-09-868-605-14\_COPY\_151\_162

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1585576

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications All: \*

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3: /cgn2\_6/ptodat/a/2/pupaa/US06\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodat/a/2/pupaa/US07\_NEW\_PUB.pep:\*

5: /cgn2\_6/ptodat/a/2/pupaa/US07\_PUBCOMB.pep:\*

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11: /cgn2\_6/ptodat/a/2/pupaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodat/a/2/pupaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodat/a/2/pupaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodat/a/2/pupaa/US10C\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodat/a/2/pupaa/US10\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodat/a/2/pupaa/US10C\_PUBCOMB.pep:\*

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18: /cgn2\_6/ptodat/a/2/pupaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodat/a/2/pupaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodat/a/2/pupaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	54	78.3	280	16 US-10-790-395-17 Sequence 17, Appli
2	54	78.3	329	9 US-9-303-510-6 Sequence 6, Appli
3	54	78.3	329	9 US-09-303-040-6 Sequence 6, Appli
4	54	78.3	329	16 US-10-790-395-7 Sequence 7, Appli
5	54	78.3	329	16 US-10-790-395-26 Sequence 26, Appli
6	51	73.9	102	9 US-09-425-762-47 Sequence 47, Appli
7	51	73.9	219	9 US-09-910-789-22 Sequence 22, Appli
8	51	73.9	246	16 US-10-314-230 Sequence 40, Appli
9	51	73.9	250	9 US-09-845-899A-5 Sequence 5, Appli
10	51	73.9	323	9 US-09-955-866-5 Sequence 5, Appli
11	51	73.9	323	9 US-09-896-738-11 Sequence 11, Appli
12	51	73.9	323	9 US-09-915-789A-16 Sequence 15, Appli
13	51	73.9	323	10 US-09-441-411-22 Sequence 22, Appli

RESULT 1

US-10-790-395-17

Sequence 17, Application US/10790396

Publication No. US20040157296A1

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin

APPLICANT: Sellins, Karen S.

TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY MOLECULES, AND USES THEREOF

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-1-CL-PC

CURRENT APPLICATION NUMBER: US/10/790,396

CURRENT FILING DATE: 2004-03-01

PRIOR APPLICATION NUMBER: US/09/646,561

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/078,765

PRIOR FILING DATE: 1998-01-19

PRIOR APPLICATION NUMBER: 09/062,597

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 17

LENGTH: 280

TYPE: PRT

ORGANISM: Canis familiaris

US-10-790-395-17

Query Match 78.3%; Score 54; DB 16; Length 280; Best Local Similarity 81.8%; Pred. No. 1.1; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSSTQGYPERQ 11

Db 158 CSSTQGYPERQ 168

RESULT 2  
 US-09-303-510-6  
 Sequence 6, Application US/09303510A  
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 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Collison, Ellen W.  
 ;  
 ; APPLICANT: Choi, InSoo  
 ;  
 ; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline  
 ; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides  
 ; FILE REFERENCE: 54954  
 ; CURRENT APPLICATION NUMBER: US/09/303,510A  
 ; CURRENT FILING DATE: 1999-04-30  
 ;  
 ; EARLIER APPLICATION NUMBER: 60/083,869  
 ; EARLIER FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 63  
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 ; SEQ ID NO: 6  
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 ; LENGTH: 329  
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 ; TYPE: PRT  
 ;  
 ; ORGANISM: Feline  
 ;  
 ; US-09-303-510-6  
 ;  
 ; Query Match  
 ; Best Local Similarity 78.3%; Score 54; DB 9; Length 329;  
 ; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 ;  
 ; QY 1 CCGTQGPEPK 11  
 ; Db 159 CCGTQGPEPK 169  
 ;  
 ;  
 ; RESULT 3  
 ; US-09-303-040-6  
 ; Sequence 6, Application US/09303040  
 ; Patent No. US20020051792A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Winslow, Barbara J.  
 ;  
 ; APPLICANT: Cochran, Mark D.  
 ;  
 ; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding  
 ; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or  
 ; FILE REFERENCE: 54957-B  
 ; CURRENT APPLICATION NUMBER: US/09/303,040  
 ; CURRENT FILING DATE: 1999-04-30  
 ;  
 ; EARLIER APPLICATION NUMBER: 60/083,870  
 ; EARLIER FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 82  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 329  
 ;  
 ; TYPE: PRT  
 ;  
 ; ORGANISM: feline CD86  
 ;  
 ; US-09-303-040-6  
 ;  
 ; Query Match  
 ; Best Local Similarity 81.8%; Score 54; DB 9; Length 329;  
 ; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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 ; QY 1 CCGTQGPEPK 11  
 ; Db 159 CCGTQGPEPK 169  
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 ; RESULT 4  
 ; US-10-790-396-7  
 ; Sequence 7, Application US/10790396  
 ; Publication No. US2004157296A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Sim, Gek-Kee  
 ;  
 ; APPLICANT: Yang, Shumin  
 ;  
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE:  
 ;  
 ; CURRENT FILING DATE: 2004-03-01  
 ;  
 ; PRIORITY NUMBER: US/09/646,561  
 ;  
 ; PRIORITY FILING DATE: 2000-09-19  
 ;  
 ; PRIORITY NUMBER: 60/078,765  
 ;  
 ; PRIORITY FILING DATE: 1998-03-19  
 ;  
 ; PRIORITY NUMBER: 09/062,597  
 ;  
 ; PRIORITY FILING DATE: 1998-04-17  
 ;  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 26  
 ; LENGTH: 332  
 ;  
 ; TYPE: PRT  
 ;  
 ; ORGANISM: Feline CD86  
 ;  
 ; US-10-790-396-7  
 ;  
 ; Query Match  
 ; Best Local Similarity 81.8%; Score 54; DB 16; Length 332;  
 ; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 ;  
 ; QY 1 CCGTQGPEPK 11  
 ; Db 159 CCGTQGPEPK 169  
 ;  
 ;  
 ; RESULT 5  
 ; US-10-790-396-26  
 ; Sequence 26, Application US/10790396  
 ; Publication No. US20040157296A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Sim, Gek-Kee  
 ;  
 ; APPLICANT: Yang, Shumin  
 ;  
 ; APPLICANT: Selina, Karen S.  
 ;  
 ; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY  
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE:  
 ;  
 ; CURRENT FILING NUMBER: US10/790,396  
 ;  
 ; PRIORITY NUMBER: US/09/646,561  
 ;  
 ; PRIORITY FILING DATE: 2000-09-19  
 ;  
 ; PRIORITY NUMBER: 60/078,765  
 ;  
 ; PRIORITY FILING DATE: 1998-03-19  
 ;  
 ; PRIORITY NUMBER: 09/062,597  
 ;  
 ; PRIORITY FILING DATE: 1998-04-17  
 ;  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 26  
 ; LENGTH: 332  
 ;  
 ; TYPE: PRT  
 ;  
 ; ORGANISM: Canis familiaris  
 ;  
 ; US-10-790-396-7  
 ;  
 ; Query Match  
 ; Best Local Similarity 81.8%; Score 54; DB 16; Length 329;  
 ; Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 ;  
 ; QY 1 CCGTQGPEPK 11  
 ; Db 159 CCGTQGPEPK 168  
 ;  
 ;  
 ; RESULT 6  
 ; US-09-425-762-47  
 ; Sequence 47, Application US/09425762  
 ; Publication No. US20030086414A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Freeman, Gordon J.  
 ;  
 ; APPLICANT: Nadel, Lee M.  
 ;  
 ; APPLICANT: Gary, Gary S.  
 ;  
 ; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Proteins, Nucleic  
 ; TITLE OF INVENTION: Uses Therefor

NUMBER OF SEQUENCES: 55  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LARIVE & COOKFIELD, LLP  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/425,762  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/479,744  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REGISTRATION NUMBER: 36 207  
 REFERENCE/DOCKET NUMBER: RP1-004CP3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400

INFORMATION FOR SEQ ID NO: 47:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 102 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein

US-09-425-762-47

RESULT 7  
 Query Match 73.9%; Score 51; DB 9; Length 102;  
 Best Local Similarity 66.7%; Pred. No. 1.3; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGTGGYPRQR 12  
 Db 24 CSSIHGYPPKK 35

US-09-915-789A-22

Sequence 22, Application US/09915789A  
 Patent No. US20020168762A1

GENERAL INFORMATION:  
 APPLICANT: Chen, Lieping  
 TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY MOLECULES  
 TITLE OF INVENTION: MOLECULES  
 FILE REFERENCE: PTO39-219001  
 CURRENT APPLICATION NUMBER: US/09/915, 789A  
 CURRENT FILING DATE: 2002-06-04  
 PRIOR APPLICATION NUMBER: US 60/220, 991  
 PRIOR FILING DATE: 2000-07-27  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 22  
 LENGTH: 219  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-915-789A-22

RESULT 8  
 Sequence 40, Application US/10334235  
 Publication No. US20040131591A1  
 GENERAL INFORMATION:  
 APPLICANT: OXFORD Biomedica (UK) Ltd.  
 APPLICANT: Kingsman, Alan  
 APPLICANT: Babbington, Christopher  
 APPLICANT: Carroll, Miles  
 APPLICANT: Ellard, Fiona  
 APPLICANT: Kingsman, Susan  
 APPLICANT: Myers, Kevin  
 APPLICANT: Lamkandra, Abigail  
 TITLE OF INVENTION: VECTOR SYSTEM  
 FILE REFERENCE: 53682000920  
 CURRENT APPLICATION NUMBER: US/10/334, 235  
 PRIOR APPLICATION NUMBER: US 10/050, 585  
 PRIOR FILING DATE: 2002-01-29  
 PRIOR APPLICATION NUMBER: PCT/GB00/04317  
 PRIOR FILING DATE: 2000-11-13  
 PRIOR APPLICATION NUMBER: US 09/445, 375  
 PRIOR FILING DATE: 1998-06-04  
 NUMBER OF SEQ ID NOS: 40  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 40  
 LENGTH: 246  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-334-235-40

Query Match 73.9%; Score 51; DB 16; Length 246;  
 Best Local Similarity 65.7%; Pred. No. 3.1; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGTGGYPRQR 12  
 Db 151 CSSIHGYPPKK 162

RESULT 9  
 Sequence 5, Application US/09845899A  
 Patent No. US20020147326A1

GENERAL INFORMATION:  
 APPLICANT: CHAIKIN, MARGERY ANN  
 APPLICANT: LYN, SALLY DOREEN PATRICIA  
 APPLICANT: SWEET, RAYMOND W.  
 APPLICANT: TRUNEB, ALEMENDED  
 TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES  
 TITLE OF INVENTION: THEREFOR  
 FILE REFERENCE: P50436  
 CURRENT APPLICATION NUMBER: US/09/845, 899A  
 CURRENT FILING DATE: 2001-04-30  
 PRIOR APPLICATION NUMBER: 09/202, 346  
 PRIOR FILING DATE: 1999-01-13  
 PRIOR APPLICATION NUMBER: US 60/043, 948  
 PRIOR FILING DATE: 1997-02-19  
 PRIOR APPLICATION NUMBER: US 60/038, 915  
 PRIOR FILING DATE: 1997-02-21  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 5  
 LENGTH: 260  
 TYPE: PRT  
 ORGANISM: HOMO SAPIENS  
 US-09-845-899A-5

Query Match 73.9%; Score 51; DB 9; Length 260;  
 Best Local Similarity 65.7%; Pred. No. 3.3; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGTGGYPRQR 12  
 Db 129 CSSIHGYPPKK 140

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RESULT 10
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIORITY APPLICATION NUMBER: US 60/220,991
; PRIORITY FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-789A-16

Query Match 73.9%; Score 51; DB 9; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C$TQGYEPQR 12
DB 151 C$SIHGYPEPK 162

RESULT 11
; APPLICANT: Sullivan, John K.
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: US/09/896,738
; Sequence 11, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: FOX, Michael
; APPLICANT: FOX, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-05-29
; PRIORITY APPLICATION NUMBER: 60/215,645
; PRIORITY FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-896-738-11

Query Match 73.9%; Score 51; DB 9; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C$TQGYEPQR 12
DB 151 C$SIHGYPEPK 162

RESULT 12
; APPLICANT: Yoshiba, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00-759-A
; CURRENT APPLICATION NUMBER: US/09/955,866
; CURRENT FILING DATE: 2001-09-19
; PRIORITY APPLICATION NUMBER: 60/233,867
; PRIORITY FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-955-866-5

Query Match 73.9%; Score 51; DB 9; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C$TQGYEPQR 12
DB 151 C$SIHGYPEPK 162

RESULT 13
; APPLICANT: Scholler, Nathalie B.
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 720033,409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-441-411-22

Query Match 73.9%; Score 51; DB 10; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C$TQGYEPQR 12
DB 151 C$SIHGYPEPK 162

RESULT 14
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIORITY APPLICATION NUMBER: US 09/747,377
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: US 09/798,586
; PRIORITY FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-789A-16

Query Match 73.9%; Score 51; DB 10; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C$TQGYEPQR 12
DB 151 C$SIHGYPEPK 162

RESULT 15
; APPLICANT: Morris, David W.
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIORITY APPLICATION NUMBER: US 09/747,377
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: US 09/798,586
; PRIORITY FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-789A-16

Query Match 73.9%; Score 51; DB 10; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C$TQGYEPQR 12
DB 151 C$SIHGYPEPK 162

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; SEQ ID NO 1080  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-1080  
Query Match 73.9%; Score 51; DB 13; length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 C~~S~~TQGY~~P~~QR 12  
Db 151 C~~S~~I~~H~~GY~~P~~E~~P~~KK 162

RESULT 15  
US-10-207-655-121  
; Sequence 121, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Lebhetter, Jeffrey A.  
; APPLICANT: Hayden Lebhetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 330069\_401C1  
; CURRENT APPLICATION NUMBER: US/10/207, 655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PugetIn version 3.0  
; SEQ ID NO 121  
; LENGTH: 323  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-121  
Query Match 73.9%; Score 51; DB 14; length 323;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 C~~S~~TQGY~~P~~QR 12  
Db 151 C~~S~~I~~H~~GY~~P~~E~~P~~KK 162

Search completed: December 15, 2004, 16:54:14  
Job time : 117.51 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:28:26 ; Search time 14.2857 Seconds

Score: 80.822 Million cell updates/sec (without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96916763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	82.6	330	2	I46691
2	51	73.9	275	2	JC7604
3	51	73.9	329	1	A48554
4	44	63.8	309	2	I49222
5	44	63.8	579	2	T30335
6	42	60.9	92	2	T18731
7	42	60.9	299	2	I46691
8	42	60.9	487	2	S65133
9	41	59.4	594	2	A45803
10	41	59.4	289	2	G0031
11	41	59.4	62	2	S70587
12	41	59.4	526	2	A37821
13	40	58.0	423	2	T29549
14	39	58.0	1273	2	T42405
15	39	56.5	215	2	C48903
16	39	56.5	323	2	AF0744
17	39	56.5	470	2	T15196
18	38	56.5	2	S59121	
19	38	55.1	100	2	PF95897
20	38	55.1	142	2	S56414
21	38	55.1	142	2	ER91374
22	38	55.1	142	2	ER86115
23	38	55.1	164	2	T15225
24	38	55.1	2	S04923	
25	38	55.1	307	2	T51863
26	38	55.1	374	2	E86226
27	38	55.1	378	2	T52026
28	38	55.1	841	2	T01046
29	38	55.1	1040	2	A57638

ALIGMENTS

RESULT 1

I46691

CD6 Precursor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 09-Jul-2004

C;Accession: I46691

R;Isoro, T.; Seto, A.

Immunogenetics 42, 217-220, 1995

A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule CD6

A;Reference number: I46689; MUID:95369849; PMID:7642234

A;Accession: I46691

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-330 <150>

A;Cross-references: UNIPROT:P42071; GB:D49842; NID:9755098; PID:BA08642.1; PID:975509

C;Superfamily: B7-2 antigen

Query Match 82.6%; Score 57; DB 2; Length 330;

Best Local Similarity 75.0%; Pred. No. 0.036; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQR 12

Db 157 CSSVQGYPEPK 168

RESULT 2

JC7604

CD86 spliced variant CD86 deltaTM isoform - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 18-Nov-2002

C;Accession: JC7604

R;Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefond, J.Y.; Delneste, Y.; Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001

A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.

A;Reference number: JC7604; MUID:21092744; PMID:1162656

A;Accession: JC7604

A;Molecule type: mRNA

A;Residues: 1-275 <149>

C;Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory molecule type.

C;Genetics: CD86 deltaTM

A;Gene: cd86deltaTM

A;Superfamily: B-lymphocyte restricted antigen B7

C;Keywords: immune response

Query Match 73.9%; Score 51; DB 2; Length 275;

Best Local Similarity 66.7%; Pred. No. 0.32; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQR 12

Db 151 CSSVQGYPEPK 162



Query Match 60.9%; Score 42; DB 2; Length 299;  
 Best Local Similarity 54.5%; Pred. No. 12; Mismatches 6;  
 Matches 6; Conservative 4; Indels 1; Gaps 0; Gaps 0;

Qy 1 CSSTQGYBPPQ 11  
 Db 161 CSASGGFPBPP 171

RESULT 8

butyrophilin - mouse (fragment)  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 15-Mar-2004  
 C;Accession: S65133  
 Rishii, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.  
 Biochim. Biophys. Acta 1245, 283-292, 1995  
 A;Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associated with the *lactose transporter*  
 A;Reference number: S65133; MUID:96125722; PMID:8541302  
 A;Accession: S65133  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-487 <ISI>  
 A;Cross-references: GB:S80542; NID:91246078; PIDN:AB3893.1; PID:91246079  
 C;Superfamily: rfp transforming protein

Query Match 60.9%; Score 42; DB 2; Length 487;  
 Best Local Similarity 63.6%; Pred. No. 20; Mismatches 7; Conservative 2; Indels 2; Gaps 0; Gaps 0;

Qy 1 CSSTQGYBPPQ 11  
 Db 128 CTSSGWWYBPPQ 138

RESULT 9

A45803  
 B-cell-restricted antigen B7 precursor - human  
 N;Alternate names: B-lymphocyte activation antigen B7  
 C;Species: *Homo sapiens* (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C;Accession: I54495; A45803  
 R;Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.  
 Immunogenetics 36, 175-181, 1992  
 A;Title: Genomic organization and chromosomal location of the human gene encoding the B-cell-restricted antigen B7  
 A;Reference number: 154495; MUID:92307753; PMID:1377173  
 A;Accession: A45803  
 A;Molecule type: DNA  
 A;Status: translated from GB/EMBL/DBJ

Query Match 59.4%; Score 41; DB 2; Length 289;  
 Best Local Similarity 60.0%; Pred. No. 17; Mismatches 6; Conservative 3; Indels 0; Gaps 0; Gaps 0;

Qy 1 CSSTQGYBPP 10  
 Db 162 CSSTGGFPBPP 171

RESULT 10

butyrophilin - red-crowned mangabey (fragment)  
 C;Species: *Cercocebus torquatus* (red-crowned mangabey, white-collared mangabey)  
 C;Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: G00031  
 R;Villingen, F.J.  
 submitted to the EMBL Data Library, January 1995  
 A;Accession: G00031  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-289 <VIL>  
 A;Cross-references: UNIPROT:Q28347; EMBL:U19833; NID:9644783; PIDN:AA86700.1; PID:9644783  
 C;Genetics; C;Superfamily: B-lymphocyte restricted antigen B7  
 Query Match 59.4%; Score 41; DB 2; Length 289;  
 Best Local Similarity 60.0%; Pred. No. 17; Mismatches 6; Conservative 3; Indels 0; Gaps 0; Gaps 0;

Qy 1 CSSTQGYBPP 10  
 Db 162 CSSTGGFPBPP 171

RESULT 11

S70587  
 butyrophilin precursor - human  
 C;Species: *Homo sapiens* (man)  
 C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S70587  
 R;Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.  
 Biochim. Biophys. Acta 1306, 1-4, 1996  
 A;Title: Cloning and sequence analysis of human butyrophilin reveals a potential receptor  
 A;Reference number: S70587; MUID:96201696; PMID:8611614  
 A;Accession: S70587  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-526 <TAY>  
 A;Cross-references: UNIPROT:Q13410; EMBL:U39576; NID:91326082; PIDN:AA50489.1; PID:91326082  
 C;Superfamily: rfp transforming protein

Query Match 59.4%; Score 41; DB 2; Length 526;  
 Best Local Similarity 63.6%; Pred. No. 32; Mismatches 7; Conservative 1; Indels 0; Gaps 0; Gaps 0;

Qy 1 CSSTQGYBPPQ 11  
 Db 164 CTSSGWWYBPPQ 174

RESULT 12

A37821  
 butyrophilin - bovine  
 C;Species: *Bos primigenius taurus* (cattle)  
 C;Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 09-Jul-2004  
 C;Accession: A37821  
 R;Jack, L.J.W.; Mather, I.H.  
 J. Biol. Chem. 265, 14481-14486, 1990  
 A;Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein  
 A;Reference number: A37821; MUID:90354411; PMID:2387867  
 A;Accession: A37821  
 A;Status: preliminary  
 A;Molecule type: mRNA

Query Match 59.4%; Score 41; DB 2; Length 288;  
 Best Local Similarity 60.0%; Pred. No. 17; Mismatches 6; Conservative 3; Indels 0; Gaps 0; Gaps 0;

A;Residues: 1-526 <JAC>  
 A;Cross-references: UNIPROT:PI8892; GB:M35551; NID:g1763685; PIDN:AB39766.1; PID:g16277  
 C;Superfamily: rfp transforming protein  
 C;Keywords: transmembrane protein

Query Match 59.4%; Score 41; DB 2; Length 526;  
 Best Local Similarity 63.6%; Pred. No. 32; Mismatches 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSSTQGPPPEQ 11  
 Db 164 CTSVGWYEPQ 174

RESULT 13

T29549

hypothetical protein ZK377.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C;Accession: T29549

R;Nhan, M.; Hawkins, J. Submitted to the EMBL Data Library, February 1997

A;Description: The sequence of *C. elegans* cosmid ZK377.

A;Reference number: Z20639

A;Accession: T29549

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-423 <NH2>

A;Experimental source: strain Bristol N2; clone ZK377.3

C;Genetics:

A;Gene: CESP:ZK377.3

A;Map position: X

A;Introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 58.0%; Score 40; DB 2; Length 423;

Best Local Similarity 60.0%; Pred. No. 38; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTQGPPPEQ 10  
 Db 153 CSPPRGFPPEP 162

RESULT 14

T242405

sax-3 protein - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T242405

R;Zallen, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A;Reference number: Z22160; MID:98117250; PMID:9458046

A;Accession: T242405

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-273 <ZAL>

A;Cross-references: UNIPROT:O44928; EMBL:AF041053; NID:g2804779; PIDN: AAC38848.1; PID:g2

C;Genetics:

A;Note: sax-3

A;Function:

A;Description: sax-3 function is required at the time of axon guidance

Query Match 58.0%; Score 40; DB 2; Length 1273;

Best Local Similarity 60.0%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTQG3PPEP 10  
 Db 154 CSPPRGFPPEP 163

A;Residues: 1-526 <JAC>

C;Superfamily: rfp transforming protein

C;Keywords: transmembrane protein

Query Match 59.4%; Score 41; DB 2; Length 526;

Best Local Similarity 63.6%; Pred. No. 32; Mismatches 3; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSSTQGPPPEQ 11  
 Db 164 CTSVGWYEPQ 174

RESULT 15

C48150

hibernation-related protein Hp-27 precursor - *Siberian chipmunk*

C;Species: *Eutamias sibiricus* (Siberian chipmunk)

C;Date: 16-Feb-1994 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: C48150; A41752

R;Takematsu, N.; Obara, K.; Kondo, J.; Kondo, N.; Shiba, T.

Mol. Cell. Biol. 13, 1516-1521, 1993

A;Title: Hibernation-associated gene regulation of plasma proteins with a collagen-like

A;Reference number: A48150; MURID:93180798; PMID:8441393

A;Accession: C48150

A;Molecule type: mRNA; protein

A;Cross-references: UNIPROT:Q06557; GB:PI2976; NID:g287471; PIDN:BA02353.1; PID:g28747

A;Note: the source is designated as Tamias sibiricus in Genbank entry TMSH27, release

A;Note: sequence extracted from NCBI backbone (NCBInet:125948; NCBI:125949)

R;Kondo, N.; Kondo, J.

J. Biol. Chem. 267, 473-478, 1992

A;Title: Identification of novel blood proteins specific for mammalian hibernation.

A;Reference number: A41752; MURID:9212696; PMID:1730610

A;Accession: A41752

A;Status: preliminary

A;Molecule type: protein

A;Residues: 31-40; A, 42-50, 'Q', 52-215 <KCON>

C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom

F1-30-Domain: signal sequence #status predicted <SIG>

F131-215/Product: hibernation-related protein Hp-27 #status experimental <MAT>

F191-214/Domain: complement C1q carboxyl-terminal homology <CIQ>

F155/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 56.5%; Score 39; DB 2; Length 215;

Best Local Similarity 77.8%; Pred. No. 28; Mismatches 7; Conservative 77.8%; Indels 0; Gaps 0;

Matches 29; Conservative 29; Indels 0; Gaps 0;

Qy 1 CSSTQGNPE 9  
 Db 29 CSSTQGNPE 37

Search completed: December 15, 2004, 16:38:02

Job time: 16.2857 secs

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6				
OM protein - protein search, using sw model					
Run on: December 15, 2004, 16:24:31 ; Search time 66:2857 Seconds	(without alignments) 104.163 Million cell updates/sec				
Title: US-09-868-605-14_COPY_151_162	104.163 Million cell updates/sec				
perfect score: 69	104.163 Million cell updates/sec				
Sequence: 1 CSSTQGYPEPQR 12	104.163 Million cell updates/sec				
Scoring table: BLOSUM62					
Gapop 10.0 , Gabext 0.5					
Searched: 1825181 seqs, 575374546 residues					
Total number of hits satisfying chosen parameters: 1825181					
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Listing first 45 summaries					
Database : UniProt-02:*	UniProt-sprot:*				
2: uniprot-trembl:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query	Match Length	DB ID	Description
1	69	100.0	325	2	002838
2	63	91.3	284	2	Q9GLJ3
3	57	82.6	330	1	CD86 RABIT
4	54	78.3	280	2	Q9TTF1
5	54	78.3	329	2	Q9TTF2
6	54	78.3	329	2	Q9XSX6
7	54	78.3	332	2	Q9GMZ7
8	54	78.3	332	2	Q95L16
9	52	75.4	275	2	Q9BD9
10	52	75.4	323	2	Q9BD8
11	52	75.4	323	2	Q9BDM4
12	52	75.4	323	2	Q9BDM9
13	51	73.9	329	1	CD86 HUMAN
14	51	73.9	329	2	AAQ89709
15	50	72.5	149	2	062810
16	50	72.5	313	2	Q5531
17	47	68.1	281	2	Q8CQE8
18	46	66.7	316	2	Q6UX12
19	46	66.7	316	2	Q7TPB4
20	46	66.7	316	2	Q8VE98
21	46	66.7	316	2	AAH5608
22	46	66.7	316	2	AAQ88709
23	46	66.7	388	2	Q8NC34
24	46	66.7	493	2	Q6P5Y4
25	46	66.7	493	2	AAH6281
26	46	66.7	533	2	Q8NCB6
27	46	66.7	534	2	Q8NB18
28	46	66.7	309	1	CD86 MOUSE
29	44	63.8	309	2	ADD25880
30	44	63.8	309	2	ADD25881
31	63.8				

RESULT 1	
ID 002838	PRELIMINARY:
AC Q02838;	PRT: 325 AA.
DT 01-JUL-1997 (TREMBLrel. 04, Created)	
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DB B7-2.	
GN Name=CD86;	
OS Sus scrofa (Pig);	
OC Bovarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Buteraria; Cetartiodactyla; Suina; Suidae; Sus;	
NCBI_TAXID=9823;	
[1]	
RP	
EX	
RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,	
RA Bothwell A.L.,	
RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human	
RT T cells: cloning, sequencing, and functional expression in human	
RT endothelial cells." J. Immunol. 157:3838-3844 (1996).	
RL EMBL; L76099; AAC61307.1; -.	
DR HSSP; P42081; INCN.	
DR InterPro; IPR007110; Ig like.	
DR Pfam; PF0003596; Ig_V.	
DR PROSITE; SW00406; IgV; 1.	
DR PROSITE; PS5034; Ig_LIKE; 1.	
SEQUENCE FROM N.A. 325 AA; 36527 MW; 998BE08137B0597D CRC64;	
Query Match 100.0%; Score 69; DB 2; Length 325;	
Best Local Similarity 100.0%; Pred. No. 0.00076;	
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY       HUMAN 1 CSSTQGYPEPQR 12	
Db 151 CSSTQGYPEPQR 162	

Aadd25882 mus muscu  
Add25883 mus muscu  
Bac37666 mus muscu  
Q61238 mus muscu  
Q64381 mus muscu  
Q63381 mus muscu  
Q91201 molluscum C  
Q91240 gallus gall  
Q91nJ8 mus muscu  
Bac30938 mus muscu  
Q62015 caenorhabdi  
P42070 oryctolagus  
Q91Yv7 mus muscu  
Q8bxrl homo sapien  
Q8ehiz rattus norv



DT 01-MAY-2000 (TREMBirel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBirel. 26, Last annotation update)  
 DE B7-2 protein.  
 GN Name=CD86;  
 OS *Canis familiaris* (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; *Canis*.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20033996; PubMed=10630300;  
 RA Yang S., Sim G.-K.;  
 RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7  
 molecules."  
 RL Immunogenetics 50:349-353(1999).  
 DR EMBL; AF106826; RAA; F12797.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR03006; Ig\_MHC.  
 DR InterPro; IPR00396; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN 1.  
 DR SEQUENCE 329 AA; 37774 MW; D96B83437BF7B73 CRC64;  
 SQ

Query Match Similarity 78.3%; Score 54; DB 2; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 0.37;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 158 C5STQGYPEPK 168

RESULT 6

Q9SX6 PRELIMINARY; PRT; 329 AA.  
 ID Q9SX6  
 AC Q9SX6;  
 DT 01-NOV-1999 (TREMBirel. 12, Last sequence update)  
 DE CD86 antigen.  
 GN Name=CD86;  
 OS *Felis silvestris catus* (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; *Felis*.  
 LL [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20180222; PubMed=10713336;  
 RA Choi I.S., Hash S.M., Winslow B.J., Collisson E.W.;  
 RT "Sequence analysis of feline B7 costimulatory molecules.";  
 RL Vet. Immunol. Immunopathol. 73:219-231(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Choi I.-S., Hash S.; Winslow B.J., Collisson E.W.;  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.  
 DR EMBL; AF05727; ADD4294.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003566; Ig\_v.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR SEQUENCE 329 AA; 37781 MW; A10621E3C00A08BB CRC64;

Query Match Similarity 78.3%; Score 54; DB 2; Length 329;  
 Best Local Similarity 81.8%; Pred. No. 0.37;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 C5STQGYPEPK 11  
 Db 159 C5STQGYPEPK 169

RESULT 7

Q9GMZ7 PRELIMINARY; PRT; 332 AA.  
 ID Q9GMZ7  
 AC Q9GMZ7;  
 DT 01-MAR-2001 (TREMBirel. 16, Created)  
 DT 01-MAR-2001 (TREMBirel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBirel. 25, Last annotation update)  
 DR B-Lymphocyte activation antigen B7-2 (CD86).  
 GN Name=CD86;  
 OS Felis silvestris catus (Cat).  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; *Felis*.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=048522; PubMed=11029611;  
 RA Nishimura Y., Shimojima M., Miyazawa T., Sato B., Nakamura K.,  
 RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;  
 RT "Molecular cloning of the cDNA encoding the feline B-Lymphocyte  
 activation antigen B7-1 (CD86) and B7-2 (CD86) homologues which  
 interact with human CTLA4-Ig";  
 RL Eur. J. Immunogenet. 27:427-430(2000).  
 DR EMBL; AB030652; BAB11688.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00405; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;

Query Match Similarity 78.3%; Score 54; DB 2; Length 332;  
 Best Local Similarity 81.8%; Pred. No. 0.38;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 C5STQGYPEPK 11  
 Db 159 C5STQGYPEPK 169

RESULT 8

Q95L16 PRELIMINARY; PRT; 332 AA.  
 ID Q95L16  
 AC Q95L16;  
 DT 01-DEC-2001 (TREMBirel. 19, Created)  
 DT 01-DEC-2001 (TREMBirel. 19, Last sequence update)  
 DT 01-DEC-2003 (TREMBirel. 25, Last annotation update)  
 DE CD86  
 GN Name=CD86;  
 OS *Felis silvestris catus* (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; *Felis*.  
 RL Vet. Immunol. Immunopathol. 73:219-231(2000).  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21390213; PubMed=11498243;  
 RA Yang S., Sellins K.S., Powell T., Stoneman B., Sim G.K.;  
 RT "Novel transcripts encoding secreted forms of feline CD80 and CD86  
 costimulatory molecules";  
 RL Vet. Immunol. Immunopathol. 81:15-21(2001).  
 DR EMBL; AY007704; AAG2342.1; -.  
 DR HSSP; P42081; INCN.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00405; IgV; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 DR SEQUENCE 332 AA; 37826 MW; 8BPC8B3667D1E3D8 CRC64;

Query Match Similarity 78.3%; Score 54; DB 2; Length 332;  
 Best Local Similarity 81.8%; Pred. No. 0.38;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 C5STQGYPEPK 11  
 Db 159 C5STQGYPEPK 169

DR |||||: ISS.  
 DR 159 CSIQGYEPK 169  
 DR GO; GO:0045404; P:positive regulation of interleukin-4 biosyn. . .; ISS.  
 DR GO; GO:0045330; P:positive regulation of T-helper 2 cell diff. . .; ISS.  
 DR GO; GO:0045411; P:positive regulation of transcription; ISS.  
 DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.  
 DR InterPro; IPR07110; Ig\_Like.  
 DR InterPro; IPR0396; Ig\_V.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR Signal.  
 KW SIGNAL 1 16 Potential.  
 FT CHAIN 17 323 AA; 37010 MW; 45B217C668A79375 CRC64;  
 SEQUENCE 323 AA; 37010 MW; 45B217C668A79375 CRC64;  
 Query Match 75.4%; Score 52; DB 2; Length 323;  
 Best Local Similarity 66.7%; Pred. No. 0.83; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 2;  
 Qy 1 CSIQGYEPK 12  
 Db 151 CSIQGYEPK 162

RESULT 10  
 Q9BDB8 PRELIMINARY; PRT; 323 AA.  
 ID Q9BDBB PRELIMINARY; PRT; 323 AA.  
 AC Q9BDB2 PRELIMINARY; PRT; 323 AA.  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DR CD86 protein precursor.  
 DR Cercopithecus aethiops (Green monkey) (grive).  
 DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 DR Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 DR Cercopithecinae; Cercopithecus.  
 DR NCBI\_TaxID:9534;  
 DR [1]  
 DR SEQUENCE FROM N.A.;  
 DR MEDLINE=2133318; PubMed=1491535;  
 DR Vullinder F., Bostik P., Mayne A.E., King C.J., Genain C.P.,  
 DR Weiss W.R., Ansari A.A.;  
 DR "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules.";  
 DR Immunogenetics 53:315-328(2001).  
 DR EMBL; AF34840; AAK75431; -.  
 DR HSSP; P42081; INCN.  
 DR GO; GO:001021; C:integral to membrane; ISS.  
 DR GO; GO:001026; P:coreceptor activity; ISS.  
 DR GO; GO:0005515; P:protein binding; ISS.  
 DR GO; GO:0016563; P:transcriptional activator activity; ISS.  
 DR GO; GO:002267; P:cell-cell signaling; ISS.  
 DR GO; GO:0045086; P:positive regulation of interleukin-4 biosyn. . .; ISS.  
 DR GO; GO:004504; P:positive regulation of interleukin-4 biosyn. . .; ISS.  
 DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.  
 DR GO; GO:0045941; P:positive regulation of transcription; ISS.  
 DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.  
 DR InterPro; IPR07110; Ig\_Like.  
 DR InterPro; IPR0396; Ig\_V.  
 DR PROSITE; SM00406; IgV; 1.  
 DR Sequence: PS00835; IG\_LIKE; 1.  
 DR InterPro; IPR0396; Ig\_V.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR Signal.  
 KW SIGNAL 1 16 Potential.  
 FT CHAIN 17 323 AA; 37045 MW; 3E43152A8FD17267 CRC64;  
 SEQUENCE 323 AA; 37045 MW; 3E43152A8FD17267 CRC64;  
 Query Match 75.4%; Score 52; DB 2; Length 323;  
 Best Local Similarity 66.7%; Pred. No. 0.83; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 2;  
 Qy 1 CSIQGYEPK 12  
 Db 151 CSIQGYEPK 162

RESULT 12



RL Immunogenetics 42:85-89 (1995).  
 RN [5]  
 RP CHARACTERIZATION.  
 RX MEDLINE:95089403; PubMed=7227824;  
 RA Larlier L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,  
 RA Okumura K., Ito D., Azuma M.;  
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.";  
 RL J. Immunol. 154:97-105 (1995).  
 RP  
 RX IDENTIFICATION AS CD86.  
 MEDLINE=94348060; PubMed=7520767;  
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,  
 RA Nagler L.M., Wakasa H., Tedder T.F.;  
 RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and activated B lymphocytes is the CD86 differentiation antigen.";  
 RL Blood 84:1430-1437 (1994).  
 CC --!- FUNCTION: Receptor involved in the costimulatory signal essential for T-lymphocyte proliferation and interleukin 2 production, by binding CD28 or CTLA-4. May play a critical role in the early events of T cell activation and costimulation of naïve T cells, such as deciding between immunity and anergy that is made by T cells within 24 hours after activation. Isoform 2 interferes with the formation of CD86 clusters, and thus acts as a negative regulator of T cell activation.  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".  
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC --!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;  
 CC Isoform=P42001-1; Sequence=Displayed;  
 CC Name=2; Synonyms=CD86 delta; CC  
 CC IsoId=P42001-2; Sequence=VSP\_009125;  
 CC --!- TISSUE SPECIFICITY: Expressed by activated B lymphocytes and monocytes.  
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC --!- DATABASE: NAME=PROK; NOTE=CD86 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see [http://www.isb-sib.ch/announce/or\\_send\\_an\\_email\\_to\\_licensee@ish-sib.ch](http://www.isb-sib.ch/announce/or_send_an_email_to_licensee@ish-sib.ch)).  
 CC  
 DR EMBL; 125259; AAAP8369.1; --!  
 DR EMBL; UD0343; AAB03814.1; --!  
 DR EMBL; UD7725; AAAB86473.1; --!  
 DR EMBL; UD7717; AAAB86473.1; JOINED.  
 DR EMBL; UD7718; AAAB86473.1; JOINED.  
 DR EMBL; UD7719; AAAB86473.1; JOINED.  
 DR EMBL; UD7721; AAAB86473.1; JOINED.  
 PIR; A48754; A48754.  
 DR PDB; JCT765.  
 DR PDB; 1185; X-ray; A; B=25-134.  
 DR PDB; INCN; X-ray; A; B=25-134.  
 DR Genew; HGNC:1705; CD86.  
 DR MLM; 601020; --!  
 DR GO; GO:00016201; C:integral membrane; IC.  
 DR GO; GO:00015026; F:coreceptor activity; NAS.  
 DR GO; GO:0005515; F:protein binding; IP1.  
 DR GO; GO:00016563; F:transcriptional activator activity; NAS.  
 DR GO; GO:007267; F:cell-cell signalling; IC.  
 DR GO; GO:0005955; F:immune response; TAS.  
 DR GO; GO:00028284; F:positive regulation of cell proliferation; TAS.  
 DR GO; GO:0045086; F:positive regulation of interleukin-2 biosyn.; NAS.  
 DR GO; GO:004540; F:positive regulation of interleukin-4 biosyn.; NAS.  
 DR GO; GO:0015630; F:positive regulation of T-helper 2 cell diff.; NAS.  
 DR GO; GO:0045941; F:positive regulation of transcription; NAS.  
 DR GO; GO:0043017; P:positive regulation of tumor necrosis factor.; NAS.  
 DR GO; GO:0042110; P:T-cell activation; IC.

DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR PROSITE; PS00290; Ig\_MHC; FALSE NEG.  
 DR 3D-structure; Alternative splicing; Glycoprotein;  
 KW Immunoglobulin domain; Polymorphism; Receptor; Signal; T-cell;  
 KW Transmembrane.  
 FT SIGNAL 1 23  
 FT CHAIN 24 329  
 FT DOMAIN 24 247  
 FT TRANSMEM 248 268  
 FT DOMAIN 269 329  
 FT DOMAIN 33 131  
 FT DOMAIN 150 225  
 FT DISULFID 40 110  
 FT DISULFID 157 218  
 FT CARBOHYD 33 33  
 FT CARBOHYD 47 47  
 FT CARBOHYD 135 135  
 FT CARBOHYD 146 146  
 FT CARBOHYD 154 154  
 FT CARBOHYD 177 177  
 FT CARBOHYD 192 192  
 FT CARBOHYD 213 213  
 FT VARSPPLIC 22 234  
 FT VARIANT 310 310  
 FT CONFLICT 27 27  
 FT STRAND 27 31  
 FT TURN 32 33  
 FT STRAND 36 37  
 FT TURN 50 51  
 FT STRAND 54 58  
 FT TURN 60 61  
 FT STRAND 64 69  
 FT TURN 70 71  
 FT STRAND 72 73  
 FT TURN 76 77  
 FT TURN 80 84  
 FT STRAND 86 89  
 FT TURN 90 93  
 FT STRAND 94 97  
 FT STRAND 107 113  
 FT STRAND 122 133  
 SQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CP7D CRC64;  
 DR  
 DR Query Match 73.9%; Score 51; DB 1; Length 329;  
 DR Best Local Similarity 66.7%; Pred. No. 1.3;  
 DR Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 DR QY 1 C5STQGPBPQR 12  
 DR Db 157 C5SIHGGPEPKK 168  
 DR  
 DR RESULT 15  
 DR AF40261  
 DR AF40261 PRELIMINARY; PRT; 329 AA.  
 DR ID AF40261  
 DR AF40261  
 DR AC  
 DR DT 02-MAR-2004 (TREMBL); 27, Created  
 DR DT 02-MAR-2004 (TREMBL); 27, Last sequence update  
 DR DT 02-MAR-2004 (TREMBL); 27, Last annotation update  
 DR DB CD86 antigen, isoform 1.  
 DR OS Homo sapiens (Human)  
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 DR OC Mammalia; Eutheria; Primata; Catarrhini; Hominoidea; Homo.  
 DR OC NCBI\_TAXID=9606;  
 DR RN [1]  
 DR RP SEQUENCE FROM N.A.  
 DR RC TISSUE-Brain.  
 DR RX MEDLINE=22388257; PubMed=1247932;  
 DR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 DR RA

RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Butzow K.H., Schaffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiroki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquaiello N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Snailius D.E., Scherch A., Schein J.B.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP  
 RC  
 TISSUE:Brain;  
 RA  
 RL Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC040281; AAH4061.1; -.  
 SQ 329 AA; 37726 MW; 65D4F3996939CF7D CRC64;  
 Query Match 73.9%; Score 51; DB 2; Length 329;  
 Best Local Similarity 66.7%; Pred. No. 1.3;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CSSI0GYBPRQR 12  
 |||||:|||:  
 Db 157 CSSIHGYBPRK 168

Search completed: December 15, 2004, 16:33:38  
 Job time : 68.2857 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 15, 2004, 16:38:07 ; search time 156 Seconds

(without alignments) 758.850 Million cell updates/sec

Title: US-09-868-605-14

Perfect score: 330

Sequence: 1 MGLSNLIFVWVLLSRAASL.....NLIKASDDNNTDFLASKL 330

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003a:\*

7: geneseqp2003b:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	325	98.5	325	3 AAY95324
2	224	67.9	325	3 AAY95321
3	76	23.0	250	2 AAW11944
4	14	4.2	329	3 AAY3228
5	14	4.2	329	3 AAY32285
6	14	4.2	329	5 AAO11734
7	14	4.2	329	5 AAU78121
8	14	4.2	332	2 AAY41079
9	13	3.9	30	3 AAY95333
10	13	3.9	30	3 AAY95327
11	13	3.9	169	2 AAY41080
12	13	3.9	280	2 AAY41078
13	13	3.9	329	2 AAY41076
14	12	3.6	29	3 AAY95331
15	12	3.6	29	3 AAY95332
16	12	3.6	29	3 AAY95330
17	12	3.6	309	2 AAW67988
18	12	3.6	309	2 AAW08468
19	12	3.6	309	2 AAW73639
20	12	3.6	309	3 AAB37085
21	12	3.6	314	2 AAR82899
22	12	3.6	339	3 AAY44113
23	12	3.6	358	3 AAY44144
24	11	3.3	3	3 AAY95329
25	10	3.0	2	3 AAB82904

ALIGNMENTS

RESULT ID	KEY	LOCATION/QUALIFIERS
1 AAY95324	Peptide	139..42
2 AAY95324	Peptide	/note= "epitope"
3 25-SBP-2000	Peptide	53..73
4 Human costimulatory molecule CD86 (B7-2).	Peptide	/note= "epitope"
5 Human costimulatory molecule CD86 (B7-2).	Peptide	101..129
6 Co-stimulatory molecule; CD86; B7-2; human; immunosuppressive; xerotransplantation; organ transplant; vaccine; epitope.	Peptide	/note= "epitope"
7 Homo sapiens.	Peptide	/note= "epitope"
8 OSA	Peptide	/note= "epitope"
9 XW	Peptide	/note= "epitope"
10 XW	Peptide	/note= "epitope"
11 XW	Peptide	/note= "epitope"
12 XW	Peptide	/note= "epitope"
13 XW	Peptide	/note= "epitope"
14 XW	Peptide	/note= "epitope"
15 XW	Peptide	/note= "epitope"
16 XW	Peptide	/note= "epitope"
17 XW	Peptide	/note= "epitope"
18 XW	Peptide	/note= "epitope"
19 XW	Peptide	/note= "epitope"
20 XW	Peptide	/note= "epitope"
21 XW	Peptide	/note= "epitope"
22 XW	Peptide	/note= "epitope"
23 XW	Peptide	/note= "epitope"
24 XW	Peptide	/note= "epitope"
25 XW	Peptide	/note= "epitope"
26 XW	Peptide	/note= "epitope"
27 XW	Peptide	/note= "epitope"
28 XW	Peptide	/note= "epitope"
29 XW	Peptide	/note= "epitope"
30 XW	Peptide	/note= "epitope"
31 XW	Peptide	/note= "epitope"
32 XW	Peptide	/note= "epitope"
33 XW	Peptide	/note= "epitope"
34 XW	Peptide	/note= "epitope"
35 XW	Peptide	/note= "epitope"
36 XW	Peptide	/note= "epitope"
37 XW	Peptide	/note= "epitope"
38 XW	Peptide	/note= "epitope"
39 XW	Peptide	/note= "epitope"
40 XW	Peptide	/note= "epitope"
41 XW	Peptide	/note= "epitope"
42 XW	Peptide	/note= "epitope"
43 XW	Peptide	/note= "epitope"
44 XW	Peptide	/note= "epitope"
45 XW	Peptide	/note= "epitope"

Novel methods for improving tolerance to a xenograft comprising immunizing a mammal with a T-cell epitope and a B-cell epitope.

Disclosure; Fig 26, 81PP; English.

The present sequence is that of human co-stimulatory molecule CD86 (B7-2). CD86 plays a key role in T cell costimulation. The invention relates to a novel strategy for inhibiting costimulation by porcine cells of

human T cells, with particular importance in the context of xerortransplantation of porcine organs. Recipients are immunised with hybrid synthetic peptides comprising a T cell epitope conjugated to sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see AAY95321-24). Peptides that induce antibodies specific for regions of costimulatory molecules involved in binding to their counter-receptors on human cells (CD28 and CD14) are capable of blocking the delivery of costimulation. Once the antibody response has been induced, the transplanted organ will recall this response due to the expression of the costimulatory molecules, thereby sustaining the response, and providing an endogenous mechanism of costimulatory blockade. The method is useful for improving the tolerance of a host to xenografts, particularly porcine pancreatic islet cells

XX Sequence 325 AA;

Query Match 98.5%; Score 325; DB 3; Length 325;

Best Local Similarity 100.0%; Pred. No. 3.5e-306; Matches 325; Conservat. 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSNILFVWLLSGASLSKQAYFNETGELPCHFTNSONSLDELVIPWQODDNLY 60

Db 1 MGLSNILFVWLLSGASLSKQAYFNETGELPCHFTNSONSLDELVIPWQODDNLY 60

Qy 61 ELYRGQEKPHVNNSKMRGTSFQDATWTRLHNQVKDKGSYQCFIHHKGPHGLVPHQ 120

Db 51 ELYRGQEKPHVNNSKMRGTSFQDATWTRLHNQVKDKGSYQCFIHHKGPHGLVPHQ 120

Qy 121 SSDSLILANSQPEINLLTHTEINLTSSTQYEPFQRMMLNKTSTEHDAM 180

Db 121 SSDSLILANSQPEINLLTHTEINLTSSTQYEPFQRMMLNKTSTEHDAM 180

Qy 181 KKSQNNITELVNNSIRVSLIPPTENVSTCVQLEPDKTFLSPCNIDAKPVPQVPP 240

Db 181 KKSQNNITELVNNSIRVSLIPPTENVSTCVQLEPDKTFLSPCNIDAKPVPQVPP 240

Qy 241 DHLWIAALIIVVVVVGMSFVTLRKKKQPGSPNIGGETKMNRAKASEQTKNRAEVH 300

Db 241 DHLWIAALIIVVVVVGMSFVTLRKKKQPGSPNIGGETKMNRAKASEQTKNRAEVH 300

Qy 301 ERSDDAQCDVNILKTAASDDNSTDF 325

Db 301 ERSDDAQCDVNILKTAASDDNSTDF 325

RESULT 2

AY95321

ID AAY95321 standard; Protein; 325 AA.

XX AAY95321;

XX AAY95321;

DT 25-SEP-2000 (First entry)

DE Pig costimulatory molecule CD86 (B7-2).

KW Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;

KW xerortransplantation; organ transplant; vaccine; epitope.

XX OS sus scrofa.

XX

KEY Location/Qualifiers

PT Peptide 17..29

PT Peptide /note= "peptide 9"

PT Peptide 21..32

PT Peptide /note= "peptide 8"

PT Peptide 32..40

PT Peptide /note= "peptide 2"

PT Peptide 76..88

PT Peptide /note= "peptide 10"

PT Peptide 81..90

PT Peptide /note= "peptide 1"

PT Peptide 94..104

PT Peptide /note= "peptide 5"

FT Peptide 109..121 /note= "peptide 3"

FT Peptide 113..121 /note= "peptide 4"

FT Peptide 151..162 /note= "peptide 6"

FT WO20037102-A2.

PR 23-OCT-1999; 98GB-00027921.

PR XX 29-JUN-2000.

PR XX 17-DEC-1999; 99WO-GB004200.

PR XX WO20037102-A2.

PR XX (MMLL-) ML LAB PLC.

PR XX Lechner RI, Rogers NJ, Dorling A;

PR XX DR WPI; 2000-42257/38.

PR XX N-4SDB; AAA49661.

PT Novel methods for improving tolerance to a xenograft comprising immunizing a mammal with a T-cell epitope and a B-cell epitope.

PT Disclosure; Fig 6; 81pp; English.

CC The present sequence is that of pig co-stimulatory molecule CD86 (B7-2), as deduced from an isolated cDNA clone (see AAY95321). CD86 plays a key role in T cell costimulation. The invention relates to a novel strategy for inhibiting costimulation by porcine cells of human T cells, with particular importance in the context of xerortransplantation of porcine organs. Recipients are immunised with hybrid synthetic peptides comprising a T cell epitope conjugated to sequences of the porcine costimulatory molecules CD80, CD86 or CD40, such as Peptides 1-10 of CD86 (see also AAY95325-33). Peptides that induce antibodies specific for regions of costimulatory molecules involved in binding to their counter-receptors on human cells (CD28 and CD14) are capable of blocking the delivery of costimulation. Once the antibody response has been induced, the transplanted organ will recall this response due to the expression of the costimulatory molecules, thereby sustaining the response, and providing an endogenous mechanism of costimulatory blockade. The method is useful for improving the tolerance of a host to xenografts, particularly porcine pancreatic islet cells

XX Sequence 325 AA;

Query Match 67.9%; Score 224; DB 3; Length 325;

Best Local Similarity 99.7%; Pred. No. 2.9e-208; Matches 324; Conservat. 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSNILFVWLLSGASLSKQAYFNETGELPCHFTNSONSLDELVIPWQODDNLY 60

Db 1 MGLSNILFVWLLSGASLSKQAYFNETGELPCHFTNSONSLDELVIPWQODDNLY 60

Qy 61 ELYRGQEKPHVNNSKMRGTSFQDATWTRLHNQVKDKGSYQCFIHHKGPHGLVPHQ 120

Db 61 ELYRGQEKPHVNNSKMRGTSFQDATWTRLHNQVKDKGSYQCFIHHKGPHGLVPHQ 120

Qy 121 SSDSLILANSQPEINLLTHTEINLTSSTQYEPFQRMMLNKTSTEHDAM 180

Db 121 SSDSLILANSQPEINLLTHTEINLTSSTQYEPFQRMMLNKTSTEHDAM 180

Qy 181 KKSQNNITELVNNSIRVSLIPPTENVSTCVQLEPDKTFLSPCNIDAKPVPQVPP 240

Db 181 KKSQNNITELVNNSIRVSLIPPTENVSTCVQLEPDKTFLSPCNIDAKPVPQVPP 240

Qy 241 DHLWIAALIIVVVVVGMSFVTLRKKKQPGSPNIGGETKMNRAKASEQTKNRAEVH 300

Db 241 DHLWIAALIIVVVVVGMSFVTLRKKKQPGSPNIGGETKMNRAKASEQTKNRAEVH 300

Qy 301 ERSDDAQCDVNILKTAASDDNSTDF 325

```

Query Match 23.0%; Score 76; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.8e-65;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 50 FWQODDNIVLIELYRGQEKPHNTSKMGRTSQDATTPLRENVQDKGSYOCFIHK 109  
 56 FWQODDNIVLIELYRGQEKPHNTSKMGRTSQDATTPLRENVQDKGSYOCFIHK 115  
 Db

Query Match 4.2%; Score 14; DB 3; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;

QY ||||| ||||| |||||  
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ||||| ||||| |||||  
 ID AAU78121 standard; protein: 329 AA.

Db 94 WTLRLHNQIKDKG 107

RESULT 5  
 AAY32285  
 ID AAY32285 standard; protein: 329 AA.

XX ||||| |||||  
 AC AAY32285;  
 DT 12-SEP-2003 (revised)  
 DT 28-FEB-2000 (first entry)

XX Feline CD86 (B7-2).  
 DE Felis catus.

XX CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator; tumour; cancer; therapy.

XX KW Felis catus.

PN W0957295-A1.

XX PD 11-NOV-1999.

XX PR 30-APR-1999; 99WKO-US009504.

XX PR 01-MAY-1998; 98US-0007111.

XX PR (SCHB ) SCHERRING-PLOUGH LTD.

XX PR (SCHE ) SCHERRING-PLOUGH VETERINARY CORP.

XX PR Winslow BJ, Cochran MD;

PT DR WPI: 2000-052155-05.

XX PR N-PSDB; AA234838.

PT Novel recombinant virus useful as immunomodulators, particularly in vaccines.

XX Disclosure; Fig 3A; 230pp; English.

RS This sequence represents feline CD86 (B7-2), as deduced from peripheral blood mononuclear cell cDNA (see AAU78128). Manipulating the expression of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86) regulates T cell proliferation and cytokine release. The invention relates to a recombinant virus that contains at least one foreign nucleic acid, inserted into a nonessential genomic region, that encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and is expressed when the recombinant virus is introduced into a suitable host. The invention also provides: a recombinant virus further comprising a foreign nucleic acid encoding an immunogen derived from a feline pathogen; recombinant viruses capable of enhancing an immune response to sequences, capable of expressing antisense sequences, capable of suppressing an immune response in a feline, e.g. for treatment of autoimmune disease or transplant rejection; and recombinant viruses expressing DNA encoding CD80 and/or CD86 used to reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 329 AA;

SQ Query Match 4.2%; Score 14; DB 5; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;

QY ||||| ||||| |||||  
 ID AAU78121 standard; protein: 329 AA.

XX AC AAU78121;  
 DT 02-JUL-2002 (first entry)

XX DE Feline CD86 protein.

RESULT 6  
 AAU7734  
 ID AAU7734 standard; protein: 329 AA.

XX AC AAU7734;  
 DT 08-AUG-2002 (first entry)

XX DE Feline CD86.

XX Cat; CD28; CD86; CTLA-4; CD86; immunogen; vaccine; viral infection; KW feline immunodeficiency disease; feline infectious peritonitis; KW feline leukaemia virus; cancer; degenerative disease; autoimmune disease; KW virucide; immunomodulator; cytostatic; immunodeficiency.

XX OS Felis catus.

PN US2002051792-A1.

XX PR 01-MAY-1998; 98US-0083870P.

XX PR 02-MAY-2002.

XX PR 30-APR-1999; 99US-00303040.

XX PR 01-MAY-1998; 98US-0083870P.

XX PR (WINS/ ) WINSLOW B J.

XX PR (COCHR/ ) COCHRAN M D.

XX PI Winslow BJ, Cochran MD;

XX PR WPI; 2002-415200/44.

XX DR N-PSDB; AAU6840.

PT New recombinant virus, useful for immunizing felines to prevent or treat feline immunodeficiency virus, comprises foreign nucleic acid encoding feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4.

PT Disclosure; Fig 3; 77pp; English.

XX The present invention relates to a recombinant virus comprising at least one foreign nucleic acid encoding a protein selected from feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4, which is capable of expression when the virus is introduced into an appropriate host. The virus can be administered to the feline in order to elicit or enhance an immune response to prevent or treat feline immunodeficiency disease, feline leukaemia, feline infectious peritonitis, cancers, degenerative and autoimmune diseases and immunodeficiency. The present sequence is a cytotoxic T lymphocyte accessory molecule described in the exemplification of the invention

XX Sequence 329 AA;

SQ Query Match 4.2%; Score 14; DB 5; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;

QY ||||| ||||| |||||  
 ID AAU78121 standard; protein: 329 AA.

XX AC AAU78121;  
 DT 02-JUL-2002 (first entry)

XX DE Feline CD86 protein.

Page 6

FT	Peptide	1	1.17	XX	Key	location/Qualifiers
FT	Peptide	18.	.30	FT	1.	.17
FT	Peptide	/note= "B7-2 amino acids 76-88"		FT	/note= "OVA323-339"	
XX		/note= "B7-2 amino acids 76-88"		FT	/note= "OVA323-339"	
PN	WO20037102-A2.			FT	/note= "B7-2 amino acids 109-121"	
XX	PD	29-JUN-2000.		XX	PN	WO20037102-A2.
XX	PF	17-DEC-1999;	99WO-GB004200.	XX	XX	XX
XX	PR	19-DEC-1998;	98GB-0002721.	XX	PR	17-DEC-1999;
XX	PR	23-OCT-1999;	99GB-00025115.	XX	PR	19-DEC-1998;
XX	PA	(MLML-)		XX	PR	98GB-0002721.
XX	PA	ML LAB PLC.		XX	PR	23-OCT-1999;
XX	PA	(MLML-)		XX	PR	99GB-00025015.
XX	PI	Lechler RI, Rogers NJ, Dorling A;		XX	PA	(MLML-)
XX	DR	WPI; 2000-442537/38.		XX	PI	ML LAB PLC.
XX	PT	Novel methods for improving tolerance to a xenograft comprising		XX	PI	Lechler RI, Rogers NJ, Dorling A;
XX	PT	immunizing a mammal with a T-cell epitope and a B-cell epitope.		XX	DR	WPI; 2000-442537/38.
XX	PS	Disclosure; Page 23; 81pp; English.		XX	XX	XX
CC	The present sequence is that of chimeric peptide 10 comprising T-cell epitope OVA23-339 from chicken egg albumin (ovalbumin) and a 3-cell epitope comprising amino acids 76-88 of pig co-stimulatory molecule CD86 (B7-2) (see AAY5321). The invention relates to a novel strategy for inhibiting costimulation by porcine cells of human T cells, with particular importance in the context of xenotransplantation of porcine organs. Recipients are immunised with hybrid synthetic peptides, such as the present peptide, comprising a T cell epitope conjugated to sequences of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that induce antibodies specific for regions of costimulatory molecules involved in binding to their counter-receptors on human cells are capable of blocking the delivery of costimulation. Once the antibody response has been induced, the transplanted organ will recall this response due to the expression of the costimulatory molecules, thereby sustaining the response, and providing an endogenous mechanism of costimulatory blockade. The method is useful for improving the tolerance of a host to xenografts, particularly porcine pancreatic islet cells. (Updated on 12-SEP-2003 to standardise OS field)		CC	PG	WPI; 2000-442537/38.	
CC	Sequence 30 AA;			CC	XX	WPI; 2000-442537/38.
CC	Query Match	3.9%	Score 13;	DB 3;	Length 30;	XX
CC	Best Local Similarity	100.0%	Pred. No.	0.00011;	Mismatches 0;	XX
CC	Matches 13;	Conservative 0;	Indels 0;	Gaps 0;		XX
QY	76 YMGRTSFQATWT	88				XX
DB	18 YMGRTSFQATWT	30				XX
RESULT 10						XX
AAV95327						XX
ID	AAV95327	standard;	peptide;	30	AA.	XX
XX						XX
AC	AAV95327;					XX
DT	12-SEP-2003	(revised)				XX
DT	25-SEP-2000	(first entry)				XX
DE	OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 3.					
XX	Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;					
XX	xerotransplantation; organ transplant; vaccine; B-cell epitope;					
KW	T-cell epitope; ovalbumin; chicken;					
KW	allergic reaction; infectious disease; tumor development; feline;					
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss;					
OS	Gallus sp.					
OS	Sus scrofa.					
OS	Chimeric.					
RESULT 11						XX
AY41080						XX
ID	AY41080	standard;	protein;	169	AA.	XX
XX						XX
AC	AY41080;					XX
XX						XX
DT	20-DEC-1999	(first entry)				XX
DE	Feline B7-2 protein (larger fragment).					
XX	B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;					
KW	T-cell epitope; ovalbumin; chicken;					
KW	allergic reaction; infectious disease; tumor development; feline;					
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss;					
XX	Gallus sp.					
OS	Sus scrofa.					
OS	Felis catus.					

PN WO9947558-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 19-MAR-1999; 99WO-US006187.  
 XX  
 PR 19-MAR-1998; 98US-0078765P.  
 PR 17-APR-1998; 98US-00062597.  
 XX  
 PA (HESK-) HESKA CORP.  
 PI Sim G, Yang S, Sellins KS;  
 XX WPI; 1999-571822/48.  
 DR DR-N-PSDB; AAZ27933.  
 XX  
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for  
 PT treating, e.g. autoimmune and atopic diseases.  
 XX  
 PS Claim 4; Page 109-111; 148PP; English.  
 XX  
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening  
 XX Sequence 280 AA;  
 XX  
 Query Match 3.9%; Score 13; DB 2; Length 280;  
 Best Local Similarity 100%; Pred. No. 0.0009; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 29 TGEELPCHFTNSON 41  
 Db 35 TGEELPCHFTNSON 47  
 XX  
 RESULT 13  
 AAY41076 AAY41076 standard; protein; 329 AA.  
 XX  
 AC AAY41076;  
 XX  
 DT 20-DEC-1999 (first entry)  
 XX  
 DE Canine B7-2 protein.  
 XX  
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;  
 KW allergic reaction; infectious disease; tumor development; canine;  
 KW graft rejection; inflammation; arthritis; atopic dermatitis.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO9947558-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 19-MAR-1999; 99WO-US006187.  
 XX  
 PR 19-MAR-1998; 98US-0078765P.  
 PR 17-APR-1998; 98US-00062597.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Sellins KS;  
 XX  
 DR WPI; 1999-571822/48.  
 DR DR-N-PSDB; AAZ27913, AAZ27915.  
 XX  
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for  
 PT treating, e.g. autoimmune and atopic diseases.  
 XX  
 PS Claim 4; Page 97-99; 148PP; English.  
 XX  
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)  
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be  
 CC expressed by standard recombinant methodology. The nucleic acid molecules  
 CC and the encoded proteins can be used for preventing or treating diseases,  
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor  
 CC development, graft rejection, inflammation, arthritic and atopic diseases  
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,  
 CC cats, cattle, sheep or pets. The products can also be used for detection,  
 CC diagnosis and drug screening

XX Sequence 329 AA;  
 SQ 3.9%; Score 13; DB 2; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 TGELPCHFTNSQN 41  
 Db 35 TGELPCHFTNSQN 47

RESULT 14  
 AA95331  
 AA95331 standard; peptide; 29 AA.  
 XX  
 AC AA95331;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 25-SEP-2000 (first entry)  
 XX OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 8.  
 XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;  
 KW xenotransplantation; organ transplant; vaccine; B-cell epitope;  
 KW T-cell epitope; ovalbumin; chicken.  
 XX Gallus sp.  
 OS Sus scrofa.  
 OS ChimERIC.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .17 /note= "OVA323-339"  
 FT 18. .29 /note= "B7-2 amino acids 21. .32"  
 XX WO20037102-A2.  
 PD 29-JUN-2000.  
 XX  
 PR 17-DEC-1999; 99WO-GB004200.  
 XX  
 PR 19-DEC-1998; 99GB-00027921.  
 XX 23-OCT-1999; 99GB-00025115.  
 PA (MLML-) ML LAB PLC.  
 XX  
 PI Lechner RI, Rogers NJ, Dorling A;  
 XX  
 DR WPI; 2000-442537/3B.  
 XX  
 PT Novel methods for improving tolerance to a xenograft comprising  
 PT immunizing a mammal with a T-cell epitope and a B-cell epitope.  
 XX  
 Disclosure: Page 23; 81pp; English.

XX The present sequence is that of chimeric peptide 8 comprising T-cell  
 CC epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell  
 CC epitope comprising amino acids 21-32 of pig co-stimulatory molecule CD86  
 CC (B7-2) (see AA95331). The invention relates to a novel strategy for  
 CC inhibiting costimulation by porcine cells of human T cells with  
 CC particular importance in the context of xenotransplantation of porcine  
 CC organs. Recipients are immunised with hybrid synthetic peptides, such as  
 CC the present peptide, comprising a T-cell epitope conjugated to sequences  
 CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that  
 CC induce antibodies specific for regions of costimulatory molecules  
 CC involved in binding to their counter-receptors on human cells are capable  
 CC of blocking the delivery of costimulation. Once the antibody response has  
 CC been induced, the transplanted organ will recall this response due to the  
 CC expression of the costimulatory molecules, thereby sustaining the  
 CC blockade. The method is useful for improving the tolerance of a host to

CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-  
 CC SEP-2003 to standardise OS field)  
 XX Sequence 29 AA;  
 SQ 3.6%; Score 12; DB 3; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 21 KSQAYFNETGEL 32  
 Db 18 KSQAYFNETGEL 29

RESULT 15  
 AA95332  
 ID AA95332 standard; peptide; 29 AA.  
 XX  
 AC AA95332;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 25-SEP-2000 (first entry)  
 XX OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 9.  
 XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;  
 KW xenotransplantation; organ transplant; vaccine; B-cell epitope;  
 KW T-cell epitope; ovalbumin; chicken.  
 XX Gallus sp.  
 OS Sus scrofa.  
 OS ChimERIC.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .17 /note= "OVA323-339"  
 FT 18. .29 /note= "B7-2 amino acids 17-29"  
 XX WO20037102-A2.  
 PD 29-JUN-2000.  
 XX  
 PR 17-DEC-1999; 99WO-GB004200.  
 XX  
 PR 19-DEC-1998; 99GB-00027921.  
 XX 23-OCT-1999; 99GB-00025015.  
 PA (MLML-) ML LAB PLC.  
 XX  
 PI Lechner RI, Rogers NJ, Dorling A;  
 XX  
 DR WPI; 2000-442537/3B.  
 XX  
 PT Novel methods for improving tolerance to a xenograft comprising  
 PT immunizing a mammal with a T-cell epitope and a B-cell epitope.  
 XX  
 Disclosure: Page 23; 81pp; English.

XX The present sequence is that of chimeric peptide 9 comprising T-cell  
 CC epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell  
 CC epitope comprising amino acids 17-29 of pig co-stimulatory molecule CD86  
 CC (B7-2) (see AA95331). The invention relates to a novel strategy for  
 CC inhibiting costimulation by porcine cells of human T cells, with  
 CC particular importance in the context of xenotransplantation of porcine  
 CC organs. Recipients are immunised with hybrid synthetic peptides, such as  
 CC the present peptide, comprising a T-cell epitope conjugated to sequences  
 CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that  
 CC induce antibodies specific for regions of costimulatory molecules  
 CC involved in binding to their counter-receptors on human cells are capable  
 CC of blocking the delivery of costimulation. Once the antibody response has  
 CC been induced, the transplanted organ will recall this response due to the  
 CC expression of the costimulatory molecules, thereby sustaining the

CC response, and providing an endogenous mechanism of costimulatory  
CC blockade. The method is useful for improving the tolerance of a host to  
CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-  
CC SEP-2003 to standardise OS field)  
XX

Sequence 29 AA;

Query Match 3.6%; Score 12; DB 3; Length 29;  
Best Local Similarity 100.0%; Prd. No. 0.001;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ASLKSQAYFNET 29

Db 18 ASLKSQAYFNET 29

Search completed: December 15, 2004, 16:56:55

Job time : 158 secs

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Gencore version 5.1.6

OM protein - protein search, using sw model

Run on: December 15, 2004, 16:50:43 ; Search time 39 Seconds

(without alignments) 561.152 Million cell updates/sec

Title: US-09-868-605-14

Perfect score: 330

Sequence: 1 MGLSNLILFVAVLILLSGAASL..... NILKTASDDNSTDFLKSKL 330

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Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AAI\*

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMBO.pep:\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

**ALIGNMENTS**

Result No.	Score	Query	Match Length	DB ID	Description
1	325	98.5	325	4	US-09-651-200-20
2	14	4.2	329	4	US-09-651-200-18
3	14	4.2	329	4	US-09-304-04-6
4	3.9	329	4	US-09-651-200-19	
5	12	3.6	329	4	US-09-928-383-10
6	12	3.6	303	4	US-09-651-200-23
7	12	3.6	303	4	US-09-441-411-15
8	12	3.6	303	4	US-09-441-411-20
9	12	3.6	309	2	US-09-450-104-4
10	12	3.6	309	3	US-09-479-744A-23
11	12	3.6	309	3	US-09-280-757A-23
12	12	3.6	309	3	US-09-205-697A-21
13	12	3.6	309	3	US-09-702-525-21
14	12	3.6	309	4	US-09-651-200-22
15	12	3.6	309	4	US-09-667-133-33
16	12	3.6	309	4	US-09-425-627-23
17	12	3.6	309	4	US-09-837-67A-21
18	12	3.6	309	3	US-09-204-132-4
19	12	3.6	309	4	US-09-441-411-13
20	12	3.6	309	4	US-09-441-411-18
21	12	3.6	309	4	US-09-441-411-24
22	12	3.6	309	5	PCT-US95-0257-21
23	12	3.6	314	3	US-08-205-697A-13
24	12	3.6	314	3	US-08-702-525-13
25	12	3.6	314	4	US-09-837-867A-13
26	12	3.6	314	4	US-09-441-411-14
27	12	3.6	314	4	US-09-441-411-19

RESULT 2  
 US-09-651-200-18  
 Sequence 18, Application US/09651200  
 Patent No. 6,429303  
 GENERAL INFORMATION:  
 APPLICANT: Green et al.  
 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B Lymphocyte Activation Antigen B-7 Family and Polypeptides Encoded Thereby  
 TITLE OF INVENTION: Polypeptides Encoded Thereby  
 FILE REFERENCE: 15966-562 (CURA-62)  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 CURRENT FILING DATE: 2000-08-30  
 PRIORITY APPLICATION NUMBER: 60/152383  
 PRIORITY FILING DATE: 1999-09-03  
 PRIORITY APPLICATION NUMBER: 60/172909  
 PRIORITY FILING DATE: 1999-12-21  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 PRIORITY FILING DATE: 2000-02-18  
 PRIORITY APPLICATION NUMBER: 60/152383  
 PRIORITY FILING DATE: 1999-09-03  
 PRIORITY APPLICATION NUMBER: 60/172909  
 PRIORITY FILING DATE: 1999-12-21  
 PRIORITY APPLICATION NUMBER: 60/183578  
 PRIORITY FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 18  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: *Felis catus*  
 US-09-651-200-18

Query Match 4.2%; Score 14; DB 4; length 329;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTIRLHNVOIKDKG 100  
 Db 94 WTIRLHNVOIKDKG 107

RESULT 3  
 US-09-303-040-5  
 Sequence 6, Application US/09303040  
 Patent No. 6558671  
 GENERAL INFORMATION:  
 APPLICANT: Witslow, Barbara J.  
 TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding Feline Cytomegalovirus and Adenovirus  
 TITLE OF INVENTION: Feline C80, Feline CD86, Feline CD28, Feline CMLA-4 or Title of Invention: Feline Interferon-gamma And Uses Thereof  
 TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof  
 FILE REFERENCE: 53957-B  
 CURRENT FILING DATE: 1999-04-30  
 EARLIER APPLICATION NUMBER: US/09/303, 040  
 EARLIER FILING DATE: 1998-05-01  
 NUMBER OF SEQ ID NOS: 82  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: *feline CD86*  
 US-09-303-040-5

Query Match 4.2%; Score 14; DB 4; length 329;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTIRLHNVOIKDKG 100  
 Db 94 WTIRLHNVOIKDKG 107

RESULT 4  
 US-09-651-200-19  
 Sequence 19, Application US/09651200  
 Patent No. 6429303  
 GENERAL INFORMATION:  
 APPLICANT: Green et al.  
 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B Lymphocyte Activation Antigen B-7 Family and Polypeptides Encoded Thereby  
 TITLE OF INVENTION: Polypeptides Encoded Thereby  
 FILE REFERENCE: 15966-562 (CURA-62)  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 CURRENT FILING DATE: 2000-08-30  
 PRIORITY APPLICATION NUMBER: 60/152383  
 PRIORITY FILING DATE: 1999-09-03  
 PRIORITY APPLICATION NUMBER: 60/172909  
 PRIORITY FILING DATE: 1999-12-21  
 PRIORITY APPLICATION NUMBER: 60/183578  
 PRIORITY FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 19  
 LENGTH: 329  
 TYPE: PRT  
 ORGANISM: *Canis familiaris*  
 US-09-651-200-19

Query Match 3.9%; Score 13; DB 4; length 329;  
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGRLPCHTNSON 41  
 Db 35 TGRLPCHTNSON 47

RESULT 5  
 US-08-928-383B-10  
 Sequence 10, Application US/08928383B  
 Patent No. 6210921  
 GENERAL INFORMATION:  
 APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson, and Marshall S. Horwitz  
 TITLE OF INVENTION: CAR, A NO. 6210921el Coxsackievirus and Adenovirus Receptor  
 TITLE OF INVENTION: Receptor  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LASHKE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/928,383B  
 FILING DATE: 12-SEP-1997  
 CLASSIFICATION:  
 APPLICATION NUMBER: US 60/026,100  
 FILING DATE: 13-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: DFN-020  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 95 amino acids

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-08-928-383B-10

Query Match 3.6%; Score 12; DB 3; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 0.00035; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNQIKD 98  
 Db 61 WTLRLHNQIKD 72

RESULT 6  
 US-09-651-200-23  
 Sequence 23, Application US/09651200  
 Patent No. 642303  
 GENERAL INFORMATION:  
 APPLICANT: Green et al  
 TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 FILE REFERENCE: 15966-562 (CURA-62)  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 CURRENT FILING DATE: 2000-08-30  
 PRIORITY NUMBER: 60/152383  
 PRIORITY FILING DATE: 1999-09-03  
 PRIORITY APPLICATION NUMBER: 60/172909  
 PRIORITY FILING DATE: 1999-12-21  
 PRIORITY APPLICATION NUMBER: 60/183578  
 PRIORITY FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 23  
 LENGTH: 303  
 TYPE: PRT  
 ORGANISM: Mus musculus

US-09-651-200-23

Query Match 3.6%; Score 12; DB 4; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNQIKD 98  
 Db 87 WTLRLHNQIKD 98

RESULT 7  
 US-09-441-411-15  
 Sequence 15, Application US/09441411  
 Patent No. 673472  
 GENERAL INFORMATION:  
 APPLICANT: Scholler, Nathalie B.  
 APPLICANT: Disis, Mary L.  
 APPLICANT: Hellstrom, Ingegerd  
 APPLICANT: Hellstrom, Karl Erik  
 TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 FILE REFERENCE: 15966-562 (CURA-62)  
 CURRENT APPLICATION NUMBER: US/09/441,411  
 CURRENT FILING DATE: 1999-11-16  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSBQ For Windows Version 4.0  
 SEQ ID NO 20  
 LENGTH: 303  
 TYPE: PRT  
 ORGANISM: Mus musculus

US-09-441-411-20

Query Match 3.6%; Score 12; DB 4; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNQIKD 98  
 Db 87 WTLRLHNQIKD 98

RESULT 8  
 US-09-441-411-20  
 Sequence 20, Application US/09441411  
 Patent No. 673472  
 GENERAL INFORMATION:  
 APPLICANT: Scholler, Nathalie B.  
 APPLICANT: Disis, Mary L.  
 APPLICANT: Hellstrom, Ingegerd  
 APPLICANT: Hellstrom, Karl Erik  
 TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
 FILE REFERENCE: 730033.409  
 CURRENT APPLICATION NUMBER: US/09/441,411  
 CURRENT FILING DATE: 1999-11-15  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSBQ For Windows Version 4.0  
 SEQ ID NO 15  
 LENGTH: 303  
 TYPE: PRT  
 ORGANISM: Mus musculus

US-09-441-411-15

Query Match 3.6%; Score 12; DB 4; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 0.001; Length 303;



APPLICANT: Nadler, Lee M.  
 TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules  
 TITLE OF INVENTION: and Uses Therefor  
 NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/205,697A  
 FILING DATE: 02-Mar-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REFERENCE NUMBER: 36 207  
 REGISTRATION NUMBER: BWI-120  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5341  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 309 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ;US-08-702-525-21  
 Query Match 3.6%; Score 12; DB 3; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 87 WTIRLHNQIKD 98  
 Db 93 WTIRLHNQIKD 104  
 RESULT 14  
 US-03-651-200-22  
 ; Sequence 22, Application US/09651200  
 ; Patent No. 642933  
 GENERAL INFORMATION:  
 ; APPLICANT: Green et al  
 ; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 ; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby  
 ; FILE REFERENCE: 15966-562 (CURA-62)  
 CURRENT APPLICATION NUMBER: US/09/651,200  
 CURRENT FILING DATE: 2000-08-30  
 PRIOR APPLICATION NUMBER: 60/152383  
 PRIOR FILING DATE: 1999-09-03  
 PRIOR APPLICATION NUMBER: 60/172909  
 PRIOR FILING DATE: 1999-12-21  
 PRIOR APPLICATION NUMBER: 60/183578  
 PRIOR FILING DATE: 2000-02-18  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 22  
 ; LENGTH: 309  
 ; TYPE: RT  
 ; ORGANISM: Mus musculus  
 ;US-09-651-200-22  
 Query Match 3.6%; Score 12; DB 4; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 87 WTIRLHNQIKD 98  
 Db 93 WTIRLHNQIKD 104  
 RESULT 15  
 US-09-667-135-33  
 ; Sequence 33, Application US/09667135  
 ; Patent No. 6521749  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vincent Ling  
 ; APPLICANT: Kyriaki Dimoussi-Joannopoulos  
 ; TITLE OF INVENTION: NOVEL GL150 MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: GNN-007  
 ; CURRENT APPLICATION NUMBER: US/09/667,135  
 ; CURRENT FILING DATE: 2000-09-21  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 33  
 RESULT 13  
 US-08-702-525-21  
 ; Sequence 21, Application US/08702525  
 ; General Information:  
 ; APPLICANT: Sharpe, Sharpe  
 ; APPLICANT: Borriello, Francescopaolo  
 ; APPLICANT: Freeman, Gordon  
 ; APPLICANT: Nadler, Lee  
 TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory  
 TITLE OF INVENTION: and Uses Therefor  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: LAHIVE & COCKFIELD  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/702,525  
 FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/205,697  
 FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/205,697  
 FILING DATE: 02-Mar-1994

LENGTH: 309  
TYPE: PRT  
ORGANISM: MUS musculus  
FEATURE:  
OTHER INFORMATION:  
US-09-667-135-33

Query Match 3.6%; Score 12; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Oy 87 WTDLRHNWQIKD 98  
Do 93 WTDLRHNWQIKD 104

Search completed: December 15, 2004, 17:01:49  
Job time : 41 secs





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FILE REFERENCE: IM-1-C1-PCT ; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/10/790,396 ; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 2004-03-01 ; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US/09/646,561 ; NUMBER OF SEQ ID NOS: 26
; PRIOR FILING DATE: 2000-09-19 ; SOFTWARE: FastSEQ for Windows Version 4.0
; PRIOR APPLICATION NUMBER: 60/078,765 ; SEQ ID NO: 15
; PRIOR FILING DATE: 1998-03-19 ; LENGTH: 303
; PRIOR APPLICATION NUMBER: 09/062,597 ; TYPE: PRT
; PRIOR FILING DATE: 1998-04-17 ; ORGANISM: Canis familiaris
; NUMBER OF SEQ ID NOS: 65 ; SEQ ID NO: 7
; SOFTWARE: PatentIn Ver. 2.0 ; LENGTH: 329
; TYPER: PRT ; US-09-441-411-15
; ORGANISM: Canis familiaris ; US-09-441-411-15
; US-10-790-396-7 ; Query Match 3.9%; Score 13; DB 16; Length 329;
; Best Local Similarity 100.0%; Pred. No. 0.00076; Mismatches 0; Indels 0; Gaps 0;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; RESULT 7 ; US-09-441-411-20
; US-10-087-192-1077 ; Sequence 1077, Application US/10087192
; Publication No. US20020182586A1 ; GENERAL INFORMATION:
; APPLICANT: Morris, David W. ; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 529452000122 ; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT APPLICATION NUMBER: US/10/087,192 ; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: US 09/747,377 ; NUMBER OF SEQ ID NOS: 26
; PRIOR FILING DATE: 2000-12-22 ; SOFTWARE: FastSEQ for Windows Version 4.0
; PRIOR APPLICATION NUMBER: US 09/798,586 ; SEQ ID NO: 20
; PRIOR FILING DATE: 2001-03-02 ; LENGTH: 303
; NUMBER OF SEQ ID NOS: 209 ; TYPE: PRT
; SOFTWARE: FastSEQ for Windows Version 4.0 ; ORGANISM: Mus musculus
; SEQ ID NO: 1077 ; LENGTH: 230
; LENGTH: 230 ; NAME/KEY: VARIANT
; TYPE: PRT ; FEATURE:
; ORGANISM: Mus musculus
; LOCATION: (1)..(230)
; OTHER INFORMATION: Xaa = Any Amino Acid ; RESULT 9
; US-10-087-192-1077 ; US-09-441-411-20
; Query Match 3.6%; Score 12; DB 13; Length 230; ; Sequence 20, Application US/09441411
; Best Local Similarity 100.0%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0; ; Publication No. US20030008342A1
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ; GENERAL INFORMATION:
; QY 87 WTLRLHNVQIKD 98 ; APPLICANT: Scholler, Nathalie B.
; DB 90 WTLRLHNVQIKD 101 ; APPLICANT: Disis, Mary L.
; ; APPLICANT: Hellstrom, Ingegard
; ; APPLICANT: Hellstrom, Karl Erik
; ; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; ; FILE REFERENCE: 730033.4091
; ; CURRENT APPLICATION NUMBER: US/10/762,128
; ; CURRENT FILING DATE: 2004-01-20
; ; PRIOR APPLICATION NUMBER: US 09/441,411
; ; PRIOR FILING DATE: 1999-11-16
; ; NUMBER OF SEQ ID NOS: 26
; ; SOFTWARE: FastSEQ for Windows Version 4.0
; ; SEQ ID NO: 15
; ; LENGTH: 303
; ; TYPE: PRT
; ; ORGANISM: Mus musculus
; ; US-10-762-128-15
; RESULT 8
; US-09-441-411-15
; Sequence 15, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegard
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.4091
; CURRENT APPLICATION NUMBER: US/10/762,128
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 09/441,411
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 15
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-762-128-15

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 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy ||||| |||||  
 Db 87 WTIRLHNQIKD 98

RESULT 11  
 US-10-762-128-20  
 Sequence 20; Application US/10762128  
 Publication No. US20040219161A1  
 GENERAL INFORMATION:  
 APPLICANT: Disis, Mary L.  
 APPLICANT: Hellstrom, Ingegerd  
 APPLICANT: Hellstrom, Karl Erik  
 TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
 FILE REFERENCE: 730033409C1  
 CURRENT APPLICATION NUMBER: US/10/762.128  
 CURRENT FILING DATE: 2004-01-20  
 PRIOR APPLICATION NUMBER: US 09/441,411  
 PRIOR FILING DATE: 1999-11-16  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 20  
 LENGTH: 303  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-762-128-20

Query Match 3.6%; Score 12; DB 17; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 87 WTIRLHNQIKD 98  
 Do 87 WTIRLHNQIKD 98

RESULT 12  
 US-09-425-762-23  
 Sequence 23; Application US/09425762  
 Publication No. US20020086414A1  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Nadler, Lee M.  
 TITLE OF INVENTION: No. 6605279el CTLA4/CD28 Ligands and  
 NUMBER OF SEQUENCES: 55  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAMIVE & COCKFIELD, LLP  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/425,762  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/479,744  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.

Query Match 3.6%; Score 12; DB 9; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 0.0068; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy ||||| |||||  
 Db 93 WTIRLHNQIKD 104

RESULT 13  
 US-09-837-867A-21  
 Sequence 21; Application US/09837867A  
 Publication No. US2002008542A1  
 GENERAL INFORMATION:  
 APPLICANT: Sharpe, Arlene H.  
 APPLICANT: Borrelli, Francescopaolo  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 TITLE OF INVENTION: No. US2002008542A1el Forms of T Cell Costimulatory  
 FILE REFERENCE: BWT-120CPADV  
 CURRENT APPLICATION NUMBER: US/09/837,867A  
 CURRENT FILING DATE: 2001-04-17  
 PRIOR APPLICATION NUMBER: 08/205,697  
 PRIOR FILING DATE: 1994-03-02  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 21  
 LENGTH: 309  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-837-867A-21

Query Match 3.6%; Score 12; DB 9; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 0.0068; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy ||||| |||||  
 Db 93 WTIRLHNQIKD 104

RESULT 14  
 US-09-441-411-13  
 Sequence 13; Application US/09441411  
 Publication No. US20030008342A1  
 GENERAL INFORMATION:  
 APPLICANT: Scholler, Nathalie B.  
 APPLICANT: Disis, Mary L.  
 APPLICANT: Hellstrom, Ingegerd  
 APPLICANT: Hellstrom, Karl Erik  
 TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES  
 FILE REFERENCE: 730033409C1  
 CURRENT APPLICATION NUMBER: US/09/441,411  
 CURRENT FILING DATE: 1999-11-16  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 13  
 LENGTH: 309  
 TYPE: PRT

ORGANISM: Mus musculus  
US-09-441-411-13

Query Match 3.6%; Score 12; DB 10; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0068; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTURLHNVQIKD 98  
Db 93 WTURLHNVQIKD 104

RESULT 15  
US-09-441-411-18

Sequence 18, Application US/09441411

Publication No. US20030008342A1

GENERAL INFORMATION:

APPLICANT: Scholler, Nathalie B.

APPLICANT: Disis, Mary L.

APPLICANT: Hellstrom, Ingegerd

APPLICANT: Hellstrom, Karl Erik

TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES

FILE REFERENCE: 730033409

CURRENT APPLICATION NUMBER: US/09/441,411

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 309

TYPE: PRT

ORGANISM: Mus musculus

US-09-441-411-18

Query Match 3.6%; Score 12; DB 10; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0068; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTURLHNVQIKD 98

Db 93 WTURLHNVQIKD 104

Search completed: December 15, 2004, 17:12:44  
Job time : 145 secs

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OM protein - protein search, using sw model.									
Run on:	December 15, 2004, 16:50:10	Search time	40	Seconds	GenCore version	5.1.6	Copyright	(c)	1993 - 2004 Compugen Ltd.
Perfect score:	330	Score:	3.0%	Length	110;	DB:	2;	2.1	outer membrane pro
Sequence:	1 MGLSNLIFVWVLLUSGASL.....	Best Local Similarity:	100.0%	Pred. No.	0.019;	S15171	3.1	7	outer membrane pro
Scoring table:	OLIGO	Comment:	This CD86 variant expressed by nonstimulated human monocytes, as a membrane	Matches:	10;	S15172	3.1	7	outer membrane pro
Gapext:	60.0	Conservative:	0;	Mismatches:	0;	T35013	2.1	3.47	probable membrane
Searched:	283416 seqs, 96216763 residues	Indels:	0;	Gaps:	0;	S15173	2	2.1	outer membrane pro
Word size :	0	Score:	3.0%	Length:	110;	S15174	2	2.1	outer membrane pro
Total number of hits satisfying chosen parameters: 283416									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Listing first 45 summaries									
Database :	PIR_79:*	PIR_79:*	PIR_79:*	PIR_79:*	PIR_79:*	PIR_79:*	PIR_79:*	PIR_79:*	PIR_79:*
1:	pix1:*	pix1:*	pix1:*	pix1:*	pix1:*	pix1:*	pix1:*	pix1:*	pix1:*
2:	pix2:*	pix2:*	pix2:*	pix2:*	pix2:*	pix2:*	pix2:*	pix2:*	pix2:*
3:	pix3:*	pix3:*	pix3:*	pix3:*	pix3:*	pix3:*	pix3:*	pix3:*	pix3:*
4:	pix4:*	pix4:*	pix4:*	pix4:*	pix4:*	pix4:*	pix4:*	pix4:*	pix4:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	% Match	Query Length	DB ID	Description	RESULT 1	149522	7	outer membrane pro
1	12	3.6	309	2	149522	Gene B7-2 protein - mouse	Gene B7-2 protein (house mouse)	7	outer membrane pro
2	10	3.0	110	2	JCT605	CD86 spliced varia	C;Species: Mus musculus (house mouse)	7	outer membrane pro
3	10	3.0	275	2	JCT604	CD86 spliced varia	C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004	7	outer membrane pro
4	10	3.0	329	1	A48754	B7-2 antigen - hum	C;Accession: 149522	7	outer membrane pro
5	10	3.0	330	2	I46691	CD86 precursor - r	J;Freeman, G. J.; Borriello, F.; Hodes, R. J.; Reiser, H.; Gibben, J. G.; Ng, J. W.; Kim, J. Exp. Med. 178, 2185-2192, 1993	7	outer membrane pro
6	8	2.4	298	2	S74562	hypothetical protein	A;Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pr	7	outer membrane pro
7	8	2.4	354	2	S60967	YGP1 protein precu	A;Reference number: 149522; MUID:94065585; PMID:7504059	7	outer membrane pro
8	8	2.4	823	2	S48394	probable membrane	A;Accession: 149522	7	outer membrane pro
9	7	2.1	20	2	I38418	HLA-A2 - human (fr	A;Status: preliminary; translated from GB/EMBL/DBJ	7	outer membrane pro
10	7	2.1	20	2	A48972	mannose-specific 1	A;Molecule type: mRNA	7	outer membrane pro
11	7	2.1	38	2	S3321	lectin - shallot	A;Cross-references: UNIPROT:P42082; GB:125506; NID:9432478; PID:943247	7	outer membrane pro
12	7	2.1	93	1	W7WJ	B7 protein - human	C;Genetics: B7-2	7	outer membrane pro
13	7	2.1	101	2	G90536	hypothetical protein	A;Gene: B7-2	7	outer membrane pro
14	7	2.1	20	2	B75616	hypothetical protein	C;Superfamily: B7-2 antigen	7	outer membrane pro
15	7	2.1	149	2	F75327	hypothetical protein	RESULT 2	149525	outer membrane pro
16	7	2.1	154	2	A81790	conserved hypothetical protein	CD86 spliced variant CD86 deltaEC isoform - human	87	outer membrane pro
17	7	2.1	176	2	T04526	hypothetical protein	C;Species: Homo sapiens (man)	WTLRHNQVQKD	outer membrane pro
18	7	2.1	194	2	A72727	probable ribosomal	C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004	98	outer membrane pro
19	7	2.1	207	2	S24364	ribosomal protein	C;Accession: JCT605	WTLRHNQVQKD	outer membrane pro
20	7	2.1	229	2	C82165	conserved hypothet	R;Magistrelli, G.; Caron, G.; Gauchat, J.-F.; Jeannin, P.; Bonnefond, J.-Y.; Delneste, Y.	93	outer membrane pro
21	7	2.1	242	2	S71757	MADS box Protein D	Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001	WTLRHNQVQKD	outer membrane pro
22	7	2.1	243	2	B99951	hypothetical protein	A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.	WTLRHNQVQKD	outer membrane pro
23	7	2.1	256	1	PRHU3	proteinase 3 (EC 3	A;Reference number: JCT605; MUID:21092744; PMID:1162656	WTLRHNQVQKD	outer membrane pro
24	7	2.1	256	2	T15383	hypothetical protein	A;Accession: JCT605	WTLRHNQVQKD	outer membrane pro
25	7	2.1	261	2	G72867	hypothetical protein	A;Residues: 1-110 <MAG>	WTLRHNQVQKD	outer membrane pro
26	7	2.1	266	1	B43326	hypothetical protein	A;Cross-references: UNIPROT:P42081	WTLRHNQVQKD	outer membrane pro
27	7	2.1	317	2	T28277	hypothetical protein	C;Comment: This CD86 variant expressed by nonstimulated human monocytes, as a membrane	WTLRHNQVQKD	outer membrane pro
28	7	2.1	324	2	S44726	outer membrane protein	C;Genetics:	WTLRHNQVQKD	outer membrane pro
29	7	2.1	331	2	S50772	hypothetical protein	A;Gene: cd86deltaEC	WTLRHNQVQKD	outer membrane pro
Query Match Similarity: 3.0%; Score: 10; DB: 2; Length: 110; Best Local Similarity: 100.0%; Pred. No.: 0.019; Mismatches: 0; Indels: 0; Gaps: 0; Comment: This CD86 variant expressed by nonstimulated human monocytes, as a membrane									
Qy	1	1	MGLSNLIFV	10		ALIGNMENTS			

Db	Db	1	MGLSNLFLVM	10
RESULT 3				
CD86	Spliced variant CD86 deltaTM isoform - human			
CD86	Spliced variant CD86 deltaTM isoform - human			
C;Species:	Homo sapiens (man)			
C;Date:	30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 18-Nov-2002			
C;Accession:	JC7604			
R;Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.				
Biochem Biophys Res Commun				
A;Title:	Identification of an alternatively spliced variant of human CD86 mRNA.			
A;Reference number:	JC7604; MUID:21092744; PMID:11162656			
A;Molecule type:	mRNA			
A;Residues:	1-275 <MAG>			
C;Comment:	This CD86 variant expressed by activated human monocytes, is a costimulatory gene.			
C;Genetics:				
A;Gene:	cdbdelatM			
C;Superfamily:	B-lymphocyte restricted antigen B7			
C;Keywords:	immune response			
Query Match	3.0%; Score 10; DB 2; Length 275;			
Best Local Similarity	100.0%; Pred. No. 0.042; 0; Mismatches 10; Conservative			
Matches	0; Indels 0; Gaps 0;			
Qy	1 MGLSNLFLVM 10			
Db				
1 MGLSNLFLVM 10				
RESULT 4				
A48754	B7-2 antigen - human			
C;Species:	Homo sapiens (man)			
C;Alternate names:	B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor			
C;Date:	10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C;Accession:	A48754; S39055			
R;Freeman, G.J.; Grubben, J.G.; Bousbouts, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, Science 262, 808-911, 1993				
A;Title:	Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell prolif.			
A;Reference number:	A48754; MUID:94053735; PMID:7694363			
A;Accession:	A48754			
A;Molecule type:	mRNA			
A;Residues:	1-29 <FRE>			
A;Cross-references:	UNIPROT:P42081; GB:125259; NID:9416368; PIDN:AA583389.1; PID:9416369			
A;Note:	it is uncertain whether Met-1 or Met-7 is the initiator			
R;Azuina, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C.				
Nature 366, 76-79, 1993				
A;Title:	B70 antigen is a second ligand for CTLA-4 and CD28.			
A;Reference number:	S39055; MUID:94050123; PMID:7694153			
A;Accession:	S39055			
A;Status:	preliminary			
A;Molecule type:	mRNA			
A;Residues:	7-29 <2GU>			
A;Cross-references:	GB:U04343; NID:9439038; PIDN:AB03814.1; PID:9439839			
A;Genes:	GDB:CD86; CD28LG2			
A;Cross-references:	GDB:433597; OMIM:601020			
C;Map position:	3q13.3-3q21			
C;Superfamily:	B7-2 antigen			
C;Keywords:	glycoprotein			
Query Match	3.0%; Score 10; DB 1; Length 329;			
Best Local Similarity	100.0%; Pred. No. 0.049; 0; Mismatches 10; Conservative			
Matches	0; Indels 0; Gaps 0;			
Qy	1 MGLSNLFLVM 10			
Db				
7 MGLSNLFLVM 16				
RESULT 5				
146691				
CD86 precursor - rabbit				
C;Species:	Oryctolagus cuniculus (domestic rabbit)			
C;Date:	14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004			
C;Accession:	I46691			
R;Isovo, T.; Sevo, A.				
Immunogenetics 42, 217-220, 1995				
A;Title:	Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule.			
A;Reference number:	I46691; MUID:9559849; PMID:762234			
A;Accession:	I46691			
A;Status:	preliminary; translated from GB/EMBL/DBJ			
A;Molecule type:	mRNA			
A;Residues:	1-350 <ISO>			
A;Cross-references:	UNIPROT:P42071; GB:D49842; NID:9755098; PIDN:BAA08642.1; PID:9755098			
C;Superfamily:	B7-2 antigen			
Query Match	3.0%; Score 10; DB 2; Length 330;			
Best Local Similarity	100.0%; Pred. No. 0.05; 0; Mismatches 10; Conservative			
Matches	0; Indels 0; Gaps 0;			
Qy	91 IIRVOIKG 100			
Db	97 IIRVOIKG 106			
RESULT 6				
574562	hypothetical protein sl10224 - Synechocystis sp. (strain PCC 6803)			
C;Species:	Synechocystis sp.			
A;Variety:	PCC 6803			
C;Date:	25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004			
C;Accession:	S74562			
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.				
O;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Wattnana, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996				
A;Title:	Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis			
S;A;Reference number:	S74322; MUID:97061201; PMID:8905231			
A;Accession:	S74562			
A;Status:	preliminary			
A;Molecule type:	DNA			
A;Residues:	1-29 <RAN>			
A;Cross-references:	UNIPROT:P72707; EMBL:D90900; GB:AB001339; NID:91651768; PIDN:BAA16			
A;Note:	the nucleotide sequence was submitted to the EMBL Data Library, June 1996			
Query Match	2.4%; Score 8; DB 2; Length 298;			
Best Local Similarity	100.0%; Pred. No. 5.4; 8; Conservative			
Matches	0; Indels 0; Gaps 0;			
Qy	13 IISGASL 20			
Db	12 IISGASL 19			
RESULT 7				
S60967	YGP1 protein precursor - yeast (Saccharomyces cerevisiae)			
N;Alternate names:	glycoprotein 38; protein N1731; protein YNL160w			
C;Species:	Saccharomyces cerevisiae			
C;Date:	15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004			
C;Accession:	S60967; A55542; S63112; S63814; S33203			
R;Naar, P.; Bacam, A.M.; Herbert, C.J.				
submitted to the EMBL Data Library, October 1995				
A;Description:	The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 tonic dystrophy kinase.			
A;Reference number:	S60958			
A;Accession:	S60967			
A;Molecule type:	DNA			
A;Residues:	1-354 <NAS>			
A;Cross-references:	UNIPROT:P38616; EMBL:X92517; NID:91050783; PID:91050792			

Mol. Cell. Biol. 14, 2740-2754, 1994  
 A;Title: Identification and characterization of a novel yeast gene: the YG1 gene product  
 A;Reference number: A56542; MUID:94167744; PMID:8139573  
 A;Accession: A5642  
 A;Molecule type: DNA  
 A;Residues: 1-46; 'D' 48-78; 'R' 80-354 <DSS>  
 A;Cross-references: GB:X73030; NID:9297484; PMID:CAA51513.1; PID:9297485  
 A;Note: authors translated the codon ACT for residue 225 as TRP  
 R;Nasr, F.; Beacom, A.M.; Herbert, C.  
 A;Reference number: S62367  
 A;Accession: S63112  
 A;Molecule type: DNA  
 A;Residues: 1-354 <NAW>  
 A;Cross-references: EMBL:Z71436; NID:91302125; PID:e239816; PID:91302126; MIPS:YNL160W  
 A;Experimental source: strain S88C  
 R;Nasr, F.; Beacom, A.M.; Herbert, C.J.  
 Yeast 12, 169-175, 1996  
 A;Title: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete dystrophy kinase.  
 A;Residue number: S63805; MUID:96287653; PMID:9686380  
 A;Accession: S63814  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-354 <NAF>  
 A;Cross-references: EMBL:X92517; NID:91050783; PMID:CAA53279.1; PID:91050792  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
 C;Genetics:  
 A;Gene: SGD:YGP1  
 A;Cross-references: SGD:S0005104; MIPS:YNL160W  
 A;Map position: 14L  
 C;Keywords: glycoprotein  
 F;1-19;Domain: signal sequence #status predicted <SIG>  
 F;20-354;Product: YGP1 protein #status predicted <MAT>  
 Query Match 2.4%; Score 8; DB 2; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 6; 3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 186 NITELYNV 193  
 ||||| |||||  
 Db 106 NITELYNV 113  
 |||||  
 RESULT 8  
 S43394  
 probable membrane protein YIL140w - yeast (Saccharomyces cerevisiae)  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 02-Dec-1994 #sequence\_revision 02-Dec-1994 #text\_change 09-Jul-2004  
 C;Accession: S43394; SS0276  
 R;Churcher, C.  
 submitted to the EMBL Data Library, September 1994  
 A;Reference number: S48310  
 A;Accession: S48394  
 A;Molecule type: DNA  
 A;Residues: 1-823 <CHU>  
 A;Cross-references: UNIPROT:P38928; GB:247047; EMBL:Z38059; NID:9603997; PID:9763206; MIM:15031509; YOR001C  
 R;Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W.  
 Yeast 10, 1503-1509, 1994  
 A;Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-  
 A;Reference number: S50275; MUID:95176709; PMID:7871890  
 A;Accession: S50275  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 80-823 <TOR>  
 A;Cross-references: EMBL:U07228; NID:9460247; PMID:AA67919.1; PID:9460249  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994  
 C;Genetics:  
 A;Gene: SGD:S004  
 A;Cross-references: SGD:S0001402; MIPS:YIL140W  
 A;Map position: 9L  
 C;Superfamily: Saccharomyces cerevisiae probable membrane protein YIL140W

C;Keywords: transmembrane protein  
 F;6-22/Domain: transmembrane #status predicted <TM1>  
 F;511-527/Domain: transmembrane #status predicted <TM2>  
 Query Match 2.4%; Score 8; DB 2; Length 823;  
 Best Local Similarity 100.0%; Pred. No. 13; 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 231 AKPPVQPP 238  
 |||||  
 Db 633 AKPPVQPP 640  
 RESULT 9  
 I38418  
 HLA-A2 - human (fragment)  
 A;Accession: I38418  
 N;Alternate names: HLA-A23  
 C;Species: Homo sapiens (man)  
 C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C;Accession: I38418; I38419  
 R;Bilas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.I.  
 A;Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in it:  
 A;Reference number: I38417; MUID:95137784; PMID:783607  
 A;Status: Preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residue: 1-20 <RE2>  
 A;Cross-references: UNIPROT:P01892; UNIPROT:O19620; EMBL:U02935; NID:9414545; PMID:AA76609.1; PID:9414545  
 A;Gene: HLA-2; HLA-23  
 A;Map position: 6p21.3  
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 Query Match 2.1%; Score 7; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.3; 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 VILLSGA 17  
 |||||  
 Db 10 VILLSGA 16  
 RESULT 10  
 A48972  
 mannose-specific lectin - ramson (fragment)  
 C;Species: Allium ursinum (ramson)  
 C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995  
 C;Accession: A48972  
 R;Yaku, H.; Goldstein, I.J.; Van Damme, E.J.; Peumans, W.J.  
 Carbohydr. Res. 229, 347-353, 1992  
 A;Title: New mannose-specific lectins from garlic (Allium sativum) and ramsons (Allium ursinum)  
 A;Reference number: A48972; MUID:93008079; PMID:1394291  
 A;Accession: A48972  
 A;Status: Preliminary  
 A;Molecule type: protein  
 A;Residues: 1-34 <KAK>  
 A;Experimental source: bulb  
 A;Note: sequence extracted from NCBI backbone (NCBIP:119584)  
 Query Match 2.1%; Score 7; DB 2; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.4; 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 55 DNVLVLE 61  
 |||||  
 Db 28 DNVLVLE 34

RESULT 11  
 S9376  
 C:Species: Allium ascalonicum (shallot)  
 C:Accession: S39376  
 R:Mo, H.; van Damme, E.J.M.; Pelemans, W.J.; Goldstein, I.J.  
 A:Chm. Biocem. Biophys. 306, 431-438, 1993  
 A:Title: Purification and characterization of a mannose-specific lectin from shallot (A1)  
 A:Accession: S39376; MUID:94029015; PMID:8215447  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-38 <MOH>  
 A:Cross-references: UNIPROT:Q9SSQ9

Query Match 2.1%; Score 7; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 22; Length 101;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 55 DNLYVE 61  
 DB 29 DNLYVE 35

RESULT 12  
 W7WL  
 C:Species: human papillomavirus type 1a  
 C:Accession: C1475  
 R:Danos, O.; Katinka, M.; Yaniv, M.  
 EMBJ. 1, 231-236, 1982  
 A:Title: Human papillomavirus 1a complete DNA sequence: a novel type of genome organization  
 A:Accession number: A90970; MUID:84182467; PMID:6325156

A:Contents: annotation  
 A:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.1%; Score 7; DB 1; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 21; Length 93;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 212 VQLEPS 218  
 DB 12 VQLEPS 18

RESULT 13  
 G0536  
 hypothetical protein NYPU\_1990 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
 C:Species: Mycoplasma pulmonis  
 C:Accession: G90536  
 R:Chambaud, I.; Heiliger, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
 Nucleic Acids Res 29, 2145-2153, 2001  
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
 A:Accession: G90536  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-101 <KUR>  
 A:Cross-references: UNIPROT:Q98R11; GB:AL445566; PID:914089612; PIDN:CAC13372.1; GSPDB:G  
 A:Experimental Source: strain UAB CTIP

RESULT 14  
 E7616  
 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C:Accession: E7516  
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A:Reference number: A75250; MUID:2003686; PMID:15567266  
 A:Accession: E7516  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-135 <WHI>  
 A:Cross-references: UNIPROT:Q9RVV9; GB:AE001862; GB:AE001825; NID:96460468; PIDN:AAF123  
 A:Experimental source: strain R1  
 C:Genetics  
 A:Gene: DRA0197  
 A:Map position: 2

Query Match 2.1%; Score 7; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 29; Length 135;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 VLLSGA 17  
 DB 17 VLLSGA 23

RESULT 15  
 F7327  
 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C:Accession: F7327  
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A:Reference number: A75250; MUID:2003686; PMID:15567266  
 A:Accession: F7327  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-149 <WHI>  
 A:Cross-references: UNIPROT:Q9RSV4; GB:AB002038; GB:AE000513; NID:96459790; PIDN:AAF115  
 A:Experimental source: strain R1  
 C:Genetics  
 A:Gene: DR2018  
 A:Map position: 1

Query Match 2.1%; Score 7; DB 2; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 31; Length 149;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 LLUSGA 18  
 DB 47 LLUSGA 53

Thu Dec 16 12:21:14 2004

us-09-868-605-14.Oligo.rpr

Search completed: December 15, 2004, 17:01:04  
Job time : 42 secs

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Copyright (c) 1993 - 2004 Compugen ltd.	GenCore version 5.1.6	Run on: December 15, 2004, 16:38:47 ; Search time 195 Seconds	968.743 Million cell updates/sec (without alignments)
OM protein - protein search, using sw model			
Perfect score: 330	US-09-868-605-14	Sequence: 1 MGLSNILFVNVLILLSGAASL. .... . NILKTASPDNSTDFLSSKL 330	
Scoring table: OLIGO	Gapop 60.0 , Gapext 60.0		
Searched: 1825181 seqs, 575374646 residues			
Word size : 0	Total number of hits satisfying chosen parameters: 1825181		
Minimum DB seq length: 0			
Maximum DB seq length: 200000000			
Post-processing: Listing first 45 summaries			
Database : UniProt_02;*	1: uniprot_sprot;*		
	2: uniprot_trembl;*		
		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
		SUMMARIES	
Result No.	Score	Query Match Length DB ID	Description
1	325	98.5 325 2 0P2838	002838 sus scrofa
2	44	13.3 44 2 Q9K75	Q9gkj5 sus scrofa
3	19	5.8 93 2 Q6QW20	Q6qm20 bos taurus
4	19	5.8 93 2 AAS8374	Aas8374 bos taurus
5	19	5.8 284 2 Q9GL33	Q9gl33 bos taurus
6	14	4.2 329 2 Q9XK6	Q9xs6 sus scrofa
7	14	4.2 32 2 Q9GM27	Q9gm27 felis silv
8	14	4.2 332 2 Q95116	Q95116 felis silv
9	13	3.9 329 2 Q9TF1	Q9tf1 canis familiaris
10	13	3.9 329 2 Q9TF2	Q9tf2 canis familiaris
11	12	3.6 309 1 CD86_MOUSE	CD86 mouse
12	12	3.6 309 1 Q9YV7	Q9yv7 mus musculus
13	12	3.6 309 2 ADD5880	Ad5880 mus musculus
14	12	3.6 309 2 ADD5881	Ad5881 mus musculus
15	12	3.6 309 2 ADD5882	Ad5882 mus musculus
16	12	3.6 309 2 ADD5883	Ad5883 mus musculus
17	12	3.6 309 2 BAC7766	Bac7766 mus musculus
18	12	3.6 314 2 Q9BDM2	Q9bdm2 cercopithecus aethiops
19	12	3.5 356 2 Q9BDM4	Q9bdm4 macaca mulatta
20	10	3.0 149 2 Q9BDM9	Q9bdm9 macaca fasciata
21	10	3.0 275 2 Q9BN9	Q9bn9 rattus norvegicus
22	10	3.0 313 2 Q9PS31	Q9ps31 rattus norvegicus
23	10	3.0 323 2 Q9BDM8	Q9bdm8 cercopithecus aethiops
24	10	3.0 323 2 Q9BDM2	Q9bdm2 cercopithecus aethiops
25	10	3.0 323 2 Q9BDM4	Q9bdm4 macaca mulatta
26	10	3.0 323 2 Q9BDM9	Q9bdm9 macaca fasciata
27	10	3.0 329 1 Q9BDM1	Q9bdm1 homo sapiens
28	10	3.0 329 1 Q9BDM2	Q9bdm2 homo sapiens
29	10	3.0 329 1 Q9BDM3	Q9bdm3 homo sapiens
30	8	2.4 108 2 Q9BDM4	Q9bdm4 rhesus macaque
31	8	2.4 108 2 Q9BDM5	Q9bdm5 lactobacillus
			ALIGNMENTS
RESULT 1			
ID 002838	PRELIMINARY;	PRT; 325 AA.	
AC 002838;			
DT 01-JUL-1997	(TRIMBurel. 04, Created)		
DT 01-JUL-1997	(TRIMBurel. 04, Last sequence update)		
DT 01-OCT-2003	(TRIMBurel. 25, Last annotation update)		
DE B7-2.			
GN Name=CD86;			
OS Sus scrofa (Pig).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
NCBI_TAXID=9823;			
RN [1]			
RP SEQUENCE FROM N.A.			
RR RX			
RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,			
RA Bothwell A.L.;			
RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human T cells: cloning, sequencing, and functional expression in human			
RT endothelial cells";			
RL J. Immunol. 157:3338-3344 (1996).			
DR EMBL; IN6099; AAB61307.1; -.			
DR HSSP; P4081; INCN.			
DR InterPro; IPR007110; Ig-like.			
DR InterPro; IPR003596; Ig_v.			
DR Pfam; PF00047; ig_1.			
DR SMART; SM00406; IgV; 1.			
DR SMART; SM00406; IgV; 1.			
DR PROSITE; PS50835; Ig_LIKE; 1.			
DR SEQ 325 AA; 36527 MN; 988BED08137B0597D CRC64;			
Query Match 98.5%; Score 325; DB 2; Length 325;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 MGLSNILFVNVLILLSGAASLQAYFNFTGELPCHFTNSQNSIDELVIFWQDQDNLVY 60			Q9bdm2 cercopithecus aethiops
Db 1 MGLSNILFVNVLILLSGAASLQAYFNFTGELPCHFTNSQNSIDELVIFWQDQDNLVY 60			Q9bdm4 macaca mulatta
QY 61 BLYRQKPKRPNRYMGRSFDAITWRLHANQIKRGSKQFIFHKGPHGVPHM 120			Q9bdm4 macaca mulatta
Db 61 BLYRQKPKRPNRYMGRSFDAITWRLHANQIKRGSKQFIFHKGPHGVPHM 120			Q9bdm9 rhesus macaque
QY 121 SSDISLILAFSPOEINLTHTEVNLTCSTQYBFORMYLNTKNTTEHDAD 180			Q9bdm9 rhesus macaque
Db 121 SSDISLILAFSPOEINLTHTEVNLTCSTQYBFORMYLNTKNTTEHDAD 180			Q9bdm1 homo sapiens
QY 181 KRSKONNTIYLYNSVRSVPIPRETNVSVCVQLEPKLILSPCNDIADKPVQPV 240			Q9bdm2 cercopithecus aethiops
Db 181 KRSKONNTIYLYNSVRSVPIPRETNVSVCVQLEPKLILSPCNDIADKPVQPV 240			Q9bdm3 macaca fasciata
QY 241 DHLWIAALLVTVVQGMFVILKRIKKQPOPSNCGETKMRKASEQTKNRAVH 300			Q9bdm4 rhesus macaque
Db 241 DHLWIAALLVTVVQGMFVILKRIKKQPOPSNCGETKMRKASEQTKNRAVH 300			Q9bdm5 lactobacillus

QY 301 ERSDAACCDVNILKTDASDNSTDF 325  
 ID 301 ERSDAACCDVNILKTDASDNSTDF 325  
 DB

RESULT 2

Q9GKJ5 PRELIMINARY; PRT; 44 AA.

ID Q9GKJ5, Created)  
 AC 01-MAR-2001 (TREMBrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBrel. 16, Last annotation update)

DB Costimulatory B-Lymphocyte antigen B7-2 (Fragment).  
 Name=CD86;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Buteria; Cetartiodactyla; Suina; Suidae; Sus.  
 DR NCBI\_TAXID=9823;  
 RN [1] SEQUENCE FROM N.A.  
 RX MEDLINE=21419000; PubMed=11528129;  
 RA Van Poucke M., Yerle M., Tuglale C., Piumi F., Genet C.,  
 Van Zeveren A., Feedman L.J.;  
 RT "Integration of porcine chromosome 13 maps.";  
 RL CytoGenet Cell Genet 93:297-303(2001).  
 DR EMBL; AF22915; AG41128.1; -.  
 FT NON-TER 1 1  
 FT NON-TER 44 44  
 SQ SEQUENCE 44 AA; 5172 MW; 07217760BB21759C CRC64;

Query Match 13.3%; Score 44; DB 2; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-36; 0; Mismatches  
 Matches 44; Conservative 0; Indels 0; Gaps 0;

QY 157 YEPORMYMLNLTNSTEHADMKQSQQNNTLYNVSIRVSLP 200  
 DB 1 YEPORMYMLNLTNSTEHADMKQSQQNNTLYNVSIRVSLP 44

RESULT 3

Q6QM20 PRELIMINARY; PRT; 93 AA.

ID Q6QM20, Created)  
 AC 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)

DB CD86 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Buteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovine; Bos.  
 RN [1] SEQUENCE FROM N.A.  
 RP NCBI\_TAXID=9913;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE-Peripheral blood;  
 RA Brooke G.P., Howard C.J., Parsons K.R.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AU291475; CACI3140.1; -.  
 DE InterPro: IPR0110; Ig-like.  
 DR InterPro: IPR0359; Ig\_v.  
 DR Pfam; PF0047; Ig; Ig\_v.  
 DR SMART; SM00406; IgV; Ig\_v.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 FT NON-TER 284 284  
 SQ SEQUENCE 284 AA; 32021 MW; 797BB6633E297841 CRC64;

Query Match 5.8%; Score 19; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-10; 0; Mismatches  
 Matches 19; Conservative 0; Indels 0; Gaps 0;

QY 237 PPVDPHILWIAILLYTVV 255  
 ID 6 PPVDPHILWIAILLYTVV 24

RESULT 4

AS48374 PRELIMINARY; PRT; 93 AA.

ID AAS48374

RESULT 5

Q9XK6 PRELIMINARY; PRT; 329 AA.

ID Q9XK6, Created)  
 AC 01-NOV-1999 (TREMBrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)

DB CD86 antigen.

GN	Name=CD85;	ID	Q95116	PRELIMINARY;	PRT;	332 AA.
OS	<i>Felis silvestris catus</i> (Cat).	AC	Q95116;			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT	01-DEC-2001 (TREMBLrel. 19, Created)			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
OX	NCBI_TaxID=9685;	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
RN	{1}	DE	CD86.			
RP	SEQUENCE FROM N.A.	GN	Name=CD86;			
RA	Choi, I.-S., Hash, S.M., Winslow, B.J., Collisson, E.W.;	OS	<i>Felis silvestris catus</i> (Cat).			
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBDB databases.	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RL	EMBL; AF157827; AAC42974.1; -.	OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
RN	[2]	OX	NCBI_TaxID=9685;			
RP	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.			
RA	Choi, I.-S., Hash, S.M., Winslow, B.J., Collisson, E.W.;	RX	Medline=21390213; PubMed=11498243;			
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBDB databases.	RA	Yang, S., Sellin, K.S., Powell, T., Stoeneman, B., Sim, G.K.;			
DR	HSSP; P42081; INCN.	RT	"Novel transcripts encoding secreted forms of feline CD80 and CD86			
DR	InterPro; IPR007110; Ig-like.	RT	costimulatory molecules."			
DR	InterPro; IPR003596; Ig_v.	RL	Vet. Immunol. Immunopathol. 81:15-21 (2001).			
DR	SMART; SM00406; IgV; 1.	DR	EMBL; AAC07704; AAC23342.1; -.			
DR	PROSITE; PS003035; Ig_LIKE; 1.	DR	HSSP; P42081; INCN.			
DR	PS003035; Ig_LIKE; 1.	DR	InterPro; IPR007110; Ig-like.			
DR	WTRLNHVQIKDKG 329 AA; 37481 MW; A10621E3C0A08BB CRC64;	DR	InterPro; IPR003596; Ig_v.			
DR	Best Local Similarity 100.0%; Pred. No. 4.6e-05; Mismatches 0; Indels 0; Gaps 0;	DR	SMART; SM00406; IgV; 1.			
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	87	WTRLNHVQIKDKG 100	PROSITE; PS00835; Ig_LIKE; 1.		
Db	94 WTRLNHVQIKDKG 107	QY	87 WTRLNHVQIKDKG 100	Sequence 332 AA; 37826 MW; 8BFC8B3667D1E3D8 CRC64;		
		Db	94 WTRLNHVQIKDKG 107	Best Local Similarity 100.0%; Pred. No. 4.7e-05; Mismatches 0; Indels 0; Gaps 0;		
RESULT 7	Q9GMZ7	PRELIMINARY;	PRT;	332 AA.		
ID	Q9GMZ7					
AC	Q9GMZ7;					
DT	01-MAR-2001 (TREMBLrel. 16, Created)	ID	Q9TMF1	PRELIMINARY;	PRT;	280 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	AC	Q9TMF1;			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DB	B-lymphocyte activation antigen B7-2 (CD86).	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
GN	Name=CD86;	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
OS	<i>Felis silvestris catus</i> (Cat).	DE	Truncated B7-2 protein.			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	GN	Name=CD86;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.	OS	<i>Canis familiaris</i> (Dog).			
OX	NCBI_TaxID=9685;	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RN	[1]	OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
RP	SEQUENCE FROM N.A.	OX				
RX	Medline=20485322; PubMed=11029611;	RN				
RA	Nishimura, Y., Shimojima, M., Miyazawa, T., Sato, E., Nakamura, K.,	[1]				
RA	Izumiya, Y., Ikeda, Y., Mikami, T., Takahashi, E.;	SEQUENCE FROM N.A.				
RT	"molecular cloning of the cDNA encoding the feline B-lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA4-1g;"	RP	Medline=0093996; PubMed=10530300;			
RT	Eur. J. Immunogenet. 27:427-430 (2000).	RT	Yang, S., Sim, G.-K.; CD80 and CD86 transcripts that encode secreted B7 molecules."			
RL	EMBL; AB030652; BAB1688.1; -.	RL	Immunogenetics 50:349-353 (1999).			
DR	HSSP; P42081; INCN.	DR	EMBL; AF06827; AAC17298.1; -.			
DR	InterPro; IPR007110; Ig-like.	DR	HSSP; P42081; INCN.			
DR	InterPro; IPR003596; Ig_v.	DR	InterPro; IPR007110; Ig-like.			
DR	SMART; SM00406; IgV; 1.	DR	InterPro; IPR003596; Ig_MHC.			
DR	PROSITE; PS00835; Ig_LIKE; 1.	DR	SMART; SM00406; IgV; 1.			
DR	SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;	DR	PROSITE; PS00390; Ig_LIKE; UNKNOWN 1.			
DR	Best Local Similarity 100.0%; Pred. No. 4.7e-05; Mismatches 0; Indels 0; Gaps 0;	DR	Sequence 280 AA; 3225 MW; 3C8B2CA4D826A7F3 CRC64;			
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY	87	WTRLNHVQIKDKG 100	Query Match 3.9%; Score 13; DB 2; Length 280;		
Db	94 WTRLNHVQIKDKG 107	QY	29 TGBLPCHFTNSQ 41	Best Local Similarity 100.0%; Pred. No. 0.00041; Mismatches 0; Indels 0; Gaps 0;		
RESULT 8	Q95116		Db	35 TGBLPCHFTNSQ 47		

RESULT 10

Q9TF2 PRELIMINARY; PRT; 329 AA.

ID Q9TF2; AC Q9TF2; DT 01-MAY-2000 (TREMBL; 13, Last sequence update)

DT 01-MAY-2000 (TREMBL; 13, Last sequence update)

DT 01-MAR-2004 (TREMBL; 26, Last annotation update)

DB B7-2 protein.

GN Name=CD86;

OC Canis familiaris (Dog).

OC Canis; familia; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Bukarvata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBI\_TAXID=9615;

RN [1] Sequence from N.A.

RX MEDLINE=20093956; PubMed=10630300;

RX Yang S., Sim G.R.;

RX "New forms of dog CD86 and CD86 transcripts that encode secreted B7 molecules";

RX Immunogenetics 50:349-353 (1999).

RX EMBL; AP106826; RAF172971; -.

RX ESSP; P42081; INCN.

RX InterPro; IPR0010; Ig-like.

RX InterPro; IPR00306; Ig\_MHC.

RX InterPro; IPR003596; Ig\_v.

RX SMART; SM00406; IgV; 1.

RX PROSITE; PS50831; Ig\_MHC; UNKNOWN 1.

RX DR 329 AA; 37774 MW; D98BB63437BF7B73 CRC64;

SEQ

Query Match 3.9%; Score 13; DB 2; Length 329;

Best Local Similarity 100.0%; Pred No. 0.00047; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

29 TGRLPCTFTNSG 41

35 TGRLPCTFTNSG 47

RESULT 11

CDD6\_MOUSE STANDARD; PRT; 309 AA.

ID CDD6\_MOUSE STANDARD; PRT; 309 AA.

AC P42082; DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (Early T cell costimulatory molecule-1) (ETC-1).

DE Name=CD86;

OS Mus musculus (Mouse).

OC Bokarvata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TAXID=10090;

RN [1] Sequence from N.A.

RX MEDLINE=94065585; PubMed=7504059;

RX Freeman G.J., Borriello F., Hodes R.J., Reiter H., Gibben J.G.,

RX Ng J.W., Kim J., Goldberg J.M., Hatchcock K., Lazlo G., Lombard L.A.,

RX Wang S., Gray G.S., Nadler L.M., Sharpe A.H.,

RT "Murine B7-2, an alternative CD144 counter-receptor that costimulates T cell proliferation and interleukin 2 production.,"

RT J. Exp. Med. 178:2185-2192 (1993).

RN [2] Sequence from N.A..

RP STRAIN=129;

RX MEDLINE=9094437; PubMed=7498929;

RX Borriello F., Oliveto J., Freeman G.J., Nadler L.M., Sharpe A.H.,

RT "Differential expression of alternate mB7-2 transcripts.,"

RN J. Immunol. 155:5490-5497 (1995).

RN [3] Sequence of 7-309 FROM N.A.

RP MEDLINE=94230971; PubMed=7513726;

RX

RA Chen C., Gault A., Shen L., Nabavi N.;

RA "Molecular cloning and expression of early T cell costimulatory molecule-1 and its characterization as B7-2 molecule.,"

RT J. Immunol. 152:4929-4936 (1994).

RL

RT -1. FUNCTION: Receptor involved in the costimulatory signal essential for T lymphocyte proliferation and interleukin 2 production, by binding CD28 or CTLA-4. May play a critical role in the early events of T cell activation and costimulation of naïve T cells, such as deciding between immunity and anergy that is made by T cells within 24 hours after activation.

CC -!- SOURCE LOCAL LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed on activated B cells.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.

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CC -----

CC DR EMBL; 12560; AAA79770.1;

CC DR EMBL; U39456; AAC52334.1;

CC DR EMBL; U39457; AAC52334.1; JOINED.

CC DR EMBL; U39461; AAC52334.1; JOINED.

CC DR EMBL; U39463; AAC52334.1; JOINED.

CC DR EMBL; U39464; AAC52334.1; JOINED.

CC DR EMBL; U39465; AAC52334.1; JOINED.

CC DR EMBL; U39466; AAC52336.1; JOINED.

CC DR EMBL; S70108; AAB30744.2; ALT\_INIT.

CC DR PIR; I49522; I49522.

CC DR HSSP; P4201; INCN.

CC DR InterPro; IPR0010; Ig\_MHC.

CC DR PROSITE; PS50831; Ig\_MHC; FALSE NEG.

CC DR InterPro; IPR00306; Ig\_MHC.

CC DR PROSITE; PS50290; Ig\_MHC; FALSE NEG.

CC KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell; Transmembrane.

FT SIGNAL 1 23

FT CHAIN 24 309

FT DOMAIN 24 244

FT TRANSMEM 245 265

FT DOMAIN 266 309

FT DOMAIN 33 128

FT DOMAIN 150 223

FT DISULFID 40 110

FT DISULFID 157 216

FT CARBOHD 33 33

FT CARBOHD 47 47

FT CARBOHD 92 92

FT CARBOHD 135 135

FT CARBOHD 146 146

FT CARBOHD 154 154

FT CARBOHD 175 175

FT CARBOHD 190 190

FT CARBOHD 231 231

FT CARBOHD 309 AA; 34665 MW; 8P58CD1FB81D5EA CRC64;

SEQ

Query Match 3.6%; Score 12; DB 1; Length 309;

Best Local Similarity 100.0%; Pred No. 0.0045; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	87	WT1RLHNQIKD	98	ID	AAD25880	PRELIMINARY;	PRT;	309 AA.
Db	93	WT1RLHNQIKD	104	AC	AAD25880;			
				DT	02-MAR-2004	(TREMBlrel. 27, Created)		
RESULT 12				DT	02-MAR-2004	(TREMBlrel. 27, Last sequence update)		
Q91YV7				DT	02-MAR-2004	(TREMBlrel. 27, Last annotation update)		
ID	Q91YV7			DE	CDB6			
AC	Q91YV7;			GN				
DT	01-DEC-2001	(TREMBlrel. 19, Created)		OS	Mus musculus (Mouse)			
DT	01-DEC-2001	(TREMBlrel. 19, Last sequence update)		OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)		OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
DE	CDB6 antigen.			NCBI_TAXID=10090;				
GN	Name=Cdb6;			RN	[1]			
OS	Mus musculus (Mouse)			RP	SEQUENCE FROM N.A.			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			RC	STRAIN=CZCII; TISSUE=spleen;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			RA	Ma. R.Z.; Teuscher C.;			
OX	NCBI_TAXID=10090;			RL	Submitted (MAY-1998); AAD2580.1; "			
OX	[1]			EMBL; A065897; AAD2580.1;				
RN	[1]			SEQUENCE	309 AA; 34665 MW;	8F58DCD1FB81D5EA CR064;		
RN				Query Match	Best Local Similarity 3.6%; Score 12; DB 2; Length 309;			
RP				Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RC	SEQUENCE FROM N.A.			QY	87	WT1RLHNQIKD	98	
RC	TISSUE=Myomata tumor metastatized to lung. MMTV-LTR/Wnt1 model.			Db	93	WT1RLHNQIKD	104	
RC	Expression driven by an MMTV-LTR enhancer.;			RESULT 14				
RA	Strausberg R.;	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.		AD25881				
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			AD25881	PRELIMINARY;	PRT;	309 AA.	
RA	SEQUENCE FROM N.A.			AC	AAD25881;			
RA	TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.			DT	02-MAR-2004	(TREMBlrel. 27, Created)		
RA	Expression driven by an MMTV-LTR enhancer.;			DT	02-MAR-2004	(TREMBlrel. 27, Last sequence update)		
RA	Strausberg R.;	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.		DT	02-MAR-2004	(TREMBlrel. 27, Last annotation update)		
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			DE	CDB6 antigen.			
RA	[2]			GN				
RA	SEQUENCE FROM N.A.			OS	Mus musculus (Mouse)			
RA	TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.			OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
RA	Expression driven by an MMTV-LTR enhancer.;			OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RA	Strausberg R.;	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.		NCBI_TAXID=10090;				
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			RN	[1]			
RA	SEQUENCE FROM N.A.			RP	SEQUENCE FROM N.A.			
RA	TISSUE=C:external side of plasma membrane; IDA.			RC	STRAIN=C57BL/6J; TISSUE=spleen;			
RA	InterPro; IPR007110; Ig-like.			RA	Ma. R.Z.; Teuscher C.;			
RA	InterPro; IPR003596; Ig_v.			RL	Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.			
DR	HSPP; P4081; INCN.			DR	EMBL; A065898; AAD2581.1; "			
DR	MGD; MGI:101773; Cdb6.			SEQUENCE	309 AA; 34665 MW;	8F58DCD1FB81D5EA CR064;		
DR	GO:000897; C:external side of plasma membrane; IDA.			Query Match	3.6%; Score 12; DB 2; Length 309;			
DR	InterPro; IPR007110; Ig-like.			Best Local Similarity	100.0%; Pred. No. 0.0045;			
DR	InterPro; IPR003596; Ig_v.			Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DR	SMART; SM00506; IgV; 1.			QY	87	WT1RLHNQIKD	98	
DR	PROSITE; PS50835; IgG_LIKE; 1.			Db	93	WT1RLHNQIKD	104	
DR	SEQUENCE; 309 AA; 34713 MW;	61593C493PCBC025 CRC64;		RESULT 15				
SQ				AD25882				
Query Match	3.6%; Score 12; DB 2; Length 309;			ID	AAD25882	PRELIMINARY;	PRT;	309 AA.
Bet. Local Similarity	100.0%; Pred. No. 0.0045;			AC	AAD25882;			
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			DT	02-MAR-2004	(TREMBlrel. 27, Created)		
QY	87	WT1RLHNQIKD	98	DT	02-MAR-2004	(TREMBlrel. 27, Last sequence update)		
Db	93	WT1RLHNQIKD	104	DT	02-MAR-2004	(TREMBlrel. 27, Last annotation update)		
RESULT 13				DE	CDB6 antigen.			
				GN				
				OS	Mus musculus (Mouse)			
				OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
				OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
				NCBI_TAXID=10090;				
				RN	[1]			
				RP	SEQUENCE FROM N.A.			

RC STRAIN=B10.S/J; TISSUE=spleen;  
RA Ma, R. Z.; Teuscher, C.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBBJ databases.  
DR EMBL; AF 005889; AA 025882; 1; -  
SEQUENCE 309 AA; 34665 MW; 8F58DC01FB81DSEA CRC64;  
SQ  
Query Match 3.6%; Score 12; DB 2; Length 309;  
Best Local Similarity 100.0%; Pred. No. 0.0045; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 87 WTLRLHNVQIKD 98  
Db ||||| ||||| |||||  
93 WTLRLHNVQIKD 104

Search completed: December 15, 2004, 17:00:18  
Job time : 199 secs